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(54) Title: PHARMACEUTICAL USE FOR SECRETED BACTERIAL EFFECTOR PROTEINS

(57) Abstract: A polypeptide conjugate contains a bacterial injectable effector protein, secreted by a modified pilus or "needle-like" structure comprising a type III or type IV secretion apparatus, and a carrier that targets the conjugate to a target cell. The effector protein is used for a variety of purposes including treatment of neurodegenerative disease, intracellular infection and diseases associated with defects of secretion.



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PHARMACEUTICAL USE OF SECRETED BACTERIAL EFFECTOR PROTEINS

5 The present invention relates to pharmaceutical use of secreted, injected bacterial effector proteins. In particular, the present invention relates to manufacture and use of such proteins and combination and conjugation of the proteins with carriers.

10 A number of deficiencies exist in the availability and suitability of neuronal therapies. At the present time, a large number of neuronal disorders have inadequate provisions for therapeutic intervention. For example there is currently no effective treatment for neuronal damage caused by ischemia or trauma. Other neurodegenerative disorders such as Motor neurone disease,
15 Alzheimer's disease, Parkinson's disease and prion disorders such as CJD are all poorly addressed by current therapies. This reflects in part the complexity of the nervous system and the difficulties in targeting suitable therapies to the specific cells affected. Neuronal repair after damage is another disorder for which there is no effective treatment.

20 A number of neurological disorders are known that arise from neuronal trauma that stimulates nerve damage due to internal processes such as apoptosis. It is known to treat such disorders using a superoxide dismutase in combination with a components that targets the enzyme to neurons. However, further active
25 compounds for treatment of neuronal disease are desired.

It is known to use type III effectors in pharmaceutical compositions.

30 US 5972899 describes a composition comprising *Shigella* IpaB, an IpaB fusion protein or a functional derivative or antagonist, or IpaB DNA for delivery to a eukaryotic cell to induce or to inhibit apoptosis. Site-specific delivery may be achieved within a targeted immunoliposome. Cell-type specificity is achieved by the incorporation of a cell-type selective monoclonal antibody into the lipid bilayer. Disadvantages associated with this delivery method include the very
35 large size, low stability and poor tissue penetration of immunoliposomes, and difficulties associated with consistent immunoliposome manufacture for therapeutic use. There is also the likelihood of a high background effect due

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to fusion of immunoliposomes with non-target cell types, caused by the inherent properties of the liposome membrane.

5 WO 01/19393 describes Type III effector proteins linked to a protein transduction domain of the HIV TAT protein. DNA constructs encoding the effector-transducer fusion protein are targeted to host cells comprising a Type III secretion system using a tissue-specific viral or plasmid vector. Upon expression in the transformed host cells, the effector-transducer conjugate is secreted and undergoes secondary redistribution and uptake by neighbouring
10 cells.

The HIV TAT transduction domain is not specific to any cell type, hence, targeting of effector is carried out solely at the DNA level. Disadvantages of targeting effector DNA (rather than targeting effector protein) include the time
15 lag for processing of effector DNA to effector protein. Where viral vectors are used, there are the risks of immunogenic effects and of the vector integrating into the genome.

20 WO 00/37493 describes *Bordetella pertussis* effector virulence genes associated with a Type III secretion system. The pathogenicity genes or encoded polypeptides are used in vaccine compositions and may be conjugated to another molecule or provided with a carrier for delivery. Pathogenicity polypeptide may be delivered via a vector directing expression of *Bordetella* pathogenicity polynucleotide in vivo.

25 WO 98/56817 describes pharmaceutical compositions comprising a non-pathogenic organism expressing the YopJ protein, and YopJ protein combined with a carrier, for delivery of YopJ to gastrointestinal cells from the gut. The delivery mechanism disclosed in this document is via the normal bacterial Type
30 III secretion system - that is, one step from bacterium to target cell.

35 WO 99/52563 describes targeting of proteins produced by recombinant *Yersinia* to the cytosol of eukaryotic cells for diagnostic/ therapeutic purposes. Fusion proteins with the YopE targeting signal are expressed in *Yersinia* cells and delivered directly to eukaryotic cells via the Type III secretion system in the presence of the SycE chaperone.

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US 5965381 describes the *in vitro* use of recombinant *Yersinia* to deliver proteins to eukaryotic cells for immune diagnostic and therapeutic purposes. The proteins are fused to a delivery sequence, recognised by the *Yersinia* Type III secretion system.

5

It is not advantageous to make use of bacteria for delivering therapeutic proteins due to the risk of eliciting an unwanted immune response.

10

The present invention has as an object the provision of new pharmaceutical compositions for a variety of uses. A further object is to provide new pharmaceutical compositions for treatment of neuronal cells.

15

Accordingly, the present invention provides new therapies based upon a new class of bacterial-derived proteins, though the scope of the invention is intended to embrace also fragments and derivatives and modifications thereof that retain the properties of the native proteins.

20

A first aspect of the invention thus lies in a pharmaceutical composition, comprising a bacterial injected effector secreted by the type III or IV secretion pathway.

25

The pharmaceutical composition can be used for treatment of a subpopulation of cells in a patient, especially for a treatment selected from promoting survival of cells, preventing damage to cells, reversing damage to cells, promoting growth of cells, inhibiting apoptosis, inhibiting release of an inflammatory mediator from cells and promoting division of cells, or for a treatment selected from inhibiting survival of cells, inhibiting growth of cells, inhibiting division of cells, promoting apoptosis, killing cells, promoting release of an inflammatory mediator from cells and regulating nitric oxide release from cells.

30

A carrier can be provided to target the effector protein to a target cell, optionally targeting the effector to a cell selected from an epithelial cell, a neuronal cell, a secretory cell, an immunological cell, an endocrine cell, an inflammatory cell, an exocrine cell, a bone cell and a cell of the cardiovascular system.

35

Another means of delivery of the effector is via a conjugate of the effector protein and the carrier, the two suitably linked by a linker. One particularly

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preferred linker is cleavable, in that it can be cleaved after entry into the target cell so as to release the effector from the carrier. This linker can be a disulphide bridge or a peptide sequence including a site for a protease found in the target cell. In another embodiment of the invention, the linker is composed of two cooperating proteins, a first cooperating protein associated with the effector and the second associated with the cell targeting component. These respective parts can be administered separately and combine *in vivo* to link the effector to the cell targeting component. An example of such a two-part linker is botulinum toxin C2₁ in cooperation with C2₂.

In one embodiment of the invention, described in more detail below, a composition comprises a neuronal cell targeting component, linked by a cleavable linker to the effector protein. Preferably, the neuronal cell targeting component comprises a first domain targeting the effector to a neuronal cell and a second domain that translocates the effector into the cytosol of the neuronal cell.

Preparation of the compositions of the invention can be by combining a type III effector protein with a pharmaceutically acceptable carrier. In such compositions, the effector protein may be on its own or may be chemically linked with a (targeting) carrier. Another preparation method is to express a DNA that encodes a polypeptide having a first region that corresponds to the effector protein and a second region that codes for the carrier. A third region, between the first and second regions, which is cleaved by a proteolytic enzyme present in the target cell is optionally included.

A specific composition of the invention, for delivery of a bacterial type III effector protein to neuronal cells, comprises:-

the effector protein; linked by a cleavable linker to
a neuronal cell targeting component, comprising a first domain that binds to a neuronal cell and a second domain that translocates the effector protein of the composition into the neuronal cell. It is preferred that the first domain is selected from (a) neuronal cell binding domains of clostridial toxins; and (b) fragments, variants and derivatives of the domains in (a) that substantially retain the neuronal cell binding activity of the domains of (a).

It is further preferred that the second domain is selected from (a) domains of clostridial neurotoxins that translocate polypeptide sequences into cells, and

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(b) fragments, variants and derivatives of the domains of (a) that substantially retain the translocating activity of the domains of (a).

5 In use of a composition of the invention for treatment of a neuronal condition, the linker is cleaved in the neuronal cell so as to release the effector protein from the targeting component, thus enabling the effector to have effect in the cell without being hindered by attachment to the targeting component.

10 Hence, also, the invention provides a method of delivering a bacterial type III effector protein to a neuronal cell comprising administering a composition of the invention.

15 The first domain may suitably be selected from (a) neuronal cell binding domains of clostridial toxins; and (b) fragments, variants and derivatives of the domains in (a) that substantially retain the neuronal cell binding activity of the domains of (a). The second domain is suitably selected from (a) domains of clostridial neurotoxins that translocate polypeptide sequences into cells, and (b) fragments, variants and derivatives of the domains of (a) that substantially retain the translocating activity of the domains of (a). The second domain is further suitably selected from:-

20 (a) a translocation domain that is not a H_N domain of a clostridial toxin and is not a fragment or derivative of a H_N domain of a clostridial toxin;

(b) a non-aggregating translocation domain as measured by size in physiological buffers;

25 (c) a H_N domain of a diphtheria toxin,

(d) a fragment or derivative of (c) that substantially retains the translocating activity of the H_N domain of a diphtheria toxin,

(e) a fusogenic peptide,

(f) a membrane disrupting peptide, and

30 (g) translocating fragments and derivatives of (e) and (f).

35 In an embodiment of the invention a construct comprises effector protein linked by a disulphide bridge to a neuronal cell targeting component comprising a first domain that binds to a neuronal cell and a second domain that translocates the effector protein into the neuronal cell. This construct is made recombinantly as a single polypeptide having a cysteine residue on the effector protein which forms a disulphide bridge with a cysteine residue on the second domain. The

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effector protein is covalently linked, initially, to the second domain. Following expression of this single polypeptide, effector protein is cleaved from the second domain leaving the effector protein linked only by the disulphide bridge to the rest of the construct.

5

Particular aspects of the invention reside in further choices for the binding and translocation domains, and one such aspect provides a non-toxic polypeptide, for delivery of the effector protein to a neuronal cell, comprising:-

10

a binding domain that binds to the neuronal cell, and
a translocation domain that translocates the effector protein into the neuronal cell,

wherein the translocation domain is not a H_N domain of a clostridial neurotoxin and is not a fragment or derivative of a H_N domain of a clostridial toxin.

15

The binding domain is suitably comprised of or derived from clostridial heavy chain fragments or modified clostridial heavy chain fragments. As used herein, the term "modified clostridial heavy chain fragment" means a polypeptide fragment that retains similar biological functions to the corresponding heavy chain of a botulinum or tetanus neurotoxin but differs in its amino acid sequence and other properties compared to the corresponding heavy chain. The invention more specifically provides such constructs that are based on fragments derived from botulinum and tetanus neurotoxins.

20

25

In a further aspect, the invention also provides a polypeptide, for delivery of a effector protein to a neuronal cell, comprising:-

a binding domain that binds to the neuronal cell, and
a translocation domain that translocates the effector protein into the neuronal cell,

wherein the resulting construct is non-aggregating.

30

35

Whether the construct is an aggregating one is usually apparent from a lack of solubility of the construct, and this may be seen upon simple visual inspection of the construct in aqueous media: non-aggregating domains result in constructs of the invention that are partially or preferably totally soluble whereas aggregating domains result in non-soluble aggregates of polypeptides having apparent sizes of many tens or even hundreds the size of a single polypeptide. Generally, the construct should be non-aggregating as measured

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by its size on gel electrophoresis, and domain sizes or apparent domain sizes thus measured should preferably be less than 1.0×10^6 daltons, more preferably less than 3.0×10^5 daltons, with the measuring being suitably carried out on native PAGE using physiological conditions.

5

A still further aspect of the invention provides a polypeptide, for delivery of a effector protein to a neuronal cell, comprising:-

a binding domain that binds to the neuronal cell, and

10

a translocation domain that translocates the effector protein into the neuronal cell,

wherein the translocation domain is selected from (1) a H_N domain of a diphtheria toxin, (2) a fragment or derivative of (1) that substantially retains the translocating activity of the H_N domain of a diphtheria toxin, (3) a fusogenic peptide, (4) a membrane disrupting peptide, (5) a H_N from botulinum toxin C_2 and (6) translocating fragments and derivatives of (3), (4) and (5).

15

It is to be noted that botulinum toxin C_2 is not a neurotoxin as it has no neuronal specificity, instead it is an enterotoxin and suitable for use in the invention to provide a non-aggregating translocation domain.

20

A yet further aspect of the invention provides a polypeptide, for delivery of a effector protein to a neuronal cell, comprising:-

a binding domain that binds to the neuronal cell, and

25

a translocation domain that translocates the effector protein into the neuronal cell,

wherein the polypeptide has reduced affinity to neutralising antibodies to tetanus toxin compared with the affinity to such antibodies of native tetanus toxin heavy chain.

30

The above aspects may singly or in any combination be exhibited by polypeptides of the invention and thus a typical preferred polypeptide of the invention (i) lacks the neurotoxic activities of botulinum and tetanus toxins, (ii) displays high affinity to neuronal cells corresponding to the affinity of a clostridial neurotoxin for those cells, (iii) contains a domain which can effect translocation across cell membranes, and (iv) occurs in a less aggregated state than the corresponding heavy chain from botulinum or tetanus toxin in physiological buffers.

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A significant advantage of the polypeptides of particular aspects of the invention is their non-aggregated state, thus rendering them more usable as soluble polypeptides. The polypeptides according to the invention generally include sequences from the H_C domains of the botulinum and tetanus neurotoxins and these are combined with functional domains from other proteins, such that the essential functions of the native heavy chains are retained. Thus, for example, the H_C domain of botulinum type F neurotoxin is fused to the translocation domain derived from diphtheria toxin to give modified clostridial heavy chain fragment. Surprisingly, such polypeptides are more useful as constructs for delivering substances to neuronal cells than are the native clostridial heavy chains.

The current invention provides constructs containing type III secreted effector proteins and optionally other functional domains that effect the specific delivery of the type III effector moiety to neuronal cells. These constructs have a variety of clinical uses for the treatment of neuronal diseases.

The type III secretion mechanism of Gram negative bacterial pathogens is a complex system used to deliver proteins to eukaryotic cells. The secretion mechanism utilises at least 10-15 essential proteins to form an injection needle that extends from the surface of the bacteria and penetrates into the host cell. The effector proteins are then trafficked across the bacterial and host membranes through the lumen of the needle and injected directly into the cell cytosol. This process involves a still undefined secretion signal and involves specific chaperone proteins that deliver the effector to the secretion machinery. The system delivers a wide range of protein effectors capable of modulating host cell function in such a way as to allow the persistence or spread of the pathogen in the host. These effectors modulate a number of signalling pathways and one pathogen may export several effectors that regulate different pathways either concurrently or during different phases of its life cycle. Type III secretion systems have been described in a wide range of pathogenic bacteria including but not restricted to :

Mammalian pathogens; *Yersinia* species (including *pestis*, *pseudotuberculosis*, *enterocolitica*) , *Salmonella* species (including *typhimurium*, *enterica*, *dublin*, *typhi*) *Escherichia coli*, *Shigella* species (e.g *flexneri*), *Pseudomonas aeruginosa*, *Chlamydia* species (e.g. *pneumoniae*, *trachomatis*), and *Bordetella* species, and *Burkholderia* species

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Plant pathogens; *Pseudomonas syringae*, *Erwinia* species, *Xanthomonas* species, *Ralstonia solanacearum*, and *Rhizobium* species

5 Insect pathogens; *Sodalis glossinidius*, *Edwardsiella ictaluri*, and *Plesiomonas* species

Effector proteins from any of these species, whether mammalian pathogens or not, have therapeutic potential for treating human or animal disease.

10 Table 1 lists a number of type III effectors that have been identified to date.

15 The type IV secretion system shows a remarkable degree of similarity to the type III system in that it forms a needle-like structure through which effector proteins are injected into the host cell cytoplasm. However, the proteins involved in the structure of the needle are different for the two systems and the effectors are also divergent. The effectors function to modulate cellular signalling to establish and maintain the intracellular niche and/or promote invasion and proliferation. The system is described as essential in a number of important bacterial pathogens including *Legionella pneumophila*, *Bordetella pertussis*, *Actinobacillus actinomycetemcomitans*, *Bartonella henselae*, *Escherichia coli*, *Helicobacter pylori*, *Coxiella burnetii*, *Brucella abortus*, *Neisseria* species and *Rickettsia* species (e.g. *proWazekii*). Similar type IV secretion systems exist in plant or invertebrate pathogens and are also a source of therapeutic agents. A number of described type IV effectors are also listed in table 1 with proposed functions.

25 The function of a variety of type III effectors has been described in recent years. Interestingly a number of effectors from different organisms have evolved to target particular signalling pathways suggesting some similarities in the mechanism of pathogenicity. The precise specificity of particular effectors may vary according to pathogen and cell type and this range of activities make them attractive candidates for therapeutic applications. Examples of some of the families of effectors useful in the present invention are described below:

35 GTPase activating proteins. YopE from *Yersinia pseudotuberculosis*, SptP from *Salmonella typhimurium* and ExoS and ExoT from *Pseudomonas aeruginosa* are all GTPase activating proteins (GAPs) for Rho family GTPases and are

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characterised by a conserved "arginine finger" domain (Black and Bliska, (2000) *Molecular Microbiology* **37**:515-527; Fu and Galan (1999) *Nature* **401**:293-297; Goehring *et al* (1999) *Journal of Biological Chemistry* **274**:36369-36372). By increasing the hydrolysis of bound GTP they promote the formation of the inactive GDP-bound of the GTPase. This acts to down-regulate the function of a range of GTPases in cells. YopE is a 23kDa effector which is translocated into the cytosol of cells during infection by *Y.pseudotuberculosis* and other strains. Studies *in vitro* have shown that it acts as a GAP for RhoA, Cdc42 and Rac1, but not for Ras (Black and Bliska, (2000) *Molecular Microbiology* **37**:515-527). A point mutation within the arginine finger motif causes a loss of GAP activity and this correlates directly with its biological activity in cells. In *in vivo* studies carried out using a cell model that mimics the normal site of *Yersinia* infection YopE appears to have a greater specificity for Cdc42 (Andor *et al* (2001) *Cellular Microbiology* **3**:301-310). The GAP activity of SptP shows greater specificity for Cdc42 and Rac1 compared to RhoA. The GAP activity of particular proteins is likely to vary for different cell types and delivery routes. SptP, ExoS and ExoT are bifunctional enzymes with additional enzymatic domains (SptP, tyrosine phosphatase; ExoS, ExoT, ADP-ribosyltransferase). In the case of ExoS this activity blocks the activation of Ras GTPase allowing a co-ordinated modulation of different signalling pathways (Henriksson *et al* (2000) *Biochemical Journal* **347**:217-222).

Guanine nucleotide exchange factor. SopE and SopE2 from *Salmonella typhimurium* and related proteins act as guanine nucleotide exchange factors (GEFs) for a range of GTPases (Hardt *et al* (1998) *Cell* **93**:815). GEFs function by enhancing the rate of replacement of bound GDP by GTP causing the activation of the GTPase. This effectively upregulates the activity of specific GTPases in the cell. Native SopE is a 240 amino acid protein which is injected into the host cell cytosol by *S.typhimurium*. The N-terminal 77 amino acids of the protein act as a secretion signal and are dispensable for the biological activity of the protein (Hardt *et al* (1998) *Cell* **93**:815). In *in vitro* studies SopE acts as a GEF for Cdc42, Rac1, Rac2, RhoA, and RhoG. Cellular GEFs show a high degree of specificity for particular GTPases and it is likely that SopE will show greater specificity *in vivo*. This specificity is likely to vary according to cell type and delivery route. The type IV effector, RalF, from *Legionella pneumophila* is a further exchange factor affecting the function of small GTPases. In this case the target is the ADP ribosylation factor (ARF) family and

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this is the first example of a bacterial effector that targets this family (Nagai *et al* (2002) *Science* **295**:679-682).

5 Covalent modification of GTPase. The type III effector YopT from *Y.pestis* and certain other *Yersinia* strains has similar effects *in vivo* to YopE (Iriarte and Cornelis (1998) *Molecular Microbiology* **29**:915-929). In HeLa cells YopT causes a shift in the electrophoretic mobility of RhoA but not Cdc-42 or Rac (Zumbihl *et al* (1999) *Journal of Biological Chemistry* **274**:29289-29293). It is still not known whether this represents a direct modification of RhoA by YopT or whether other cellular factors are involved. The specificity of YopT for RhoA offers significant therapeutic possibilities.

15 Regulation of cell signalling via protein kinase and phosphatase. YopO/YpkA from *Yersinia* spp are protein kinase related to eukaryotic serine/threonine kinases (Galyov *et al* (1993) *Nature* **361**:730-732). YopO/YpkA causes a similar cell rounding to that observed for other effectors such as YopE suggesting a role in modulating GTPase function. The small GTPases RhoA and Rac1 have been shown to bind to YopO and YpkA suggesting that these are the intracellular targets for the kinase (Barz C *et al* (2000) *FEBS Letters* **482**:139-143). The type IV effector CagA from *Helicobacter pylori* also affects the cytoskeleton of infected cells and its activity is dependent on its phosphorylation by intracellular kinases. CagA functions via the SHP-2 tyrosine phosphatase to modulate downstream signalling.

25 Inositol phosphatases. SigD from *Salmonella typhimurium*, SopB from *S.dublin* and IpgD from *Shigella flexneri* are all putative inositol phosphatases. In intestinal cells SopB causes an accumulation of inositol 1,4,5,6, tetrakisphosphate. Mutations in active site of SopB abolishes both its phosphatase activity and the accumulation of inositol tetrakisphosphate (Norris *et al* (1998) *Proceedings of the National Academy of Science U.S.A* **95**:14057-14059). SopB appears to hydrolyse a wide range of inositol and phosphatidylinositol phosphates *in vitro* although its precise intracellular target remains to be defined (Eckmann *et al* (1997) *Proceedings of the National Academy of Science U.S.A* **94**:14456-14460). SigD appears to have a different specificity *in vivo* as it does not lead to an increase in the levels of inositol 1,4,5,6, tetrakisphosphate (Eckmann *et al* (1997)). Although again the precise intracellular target has not been defined, SigD has been shown to lead to the

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activation of Akt /Protein kinase B in epithelial cells (Steele-Mortimer (2000) *Journal of Biological Chemistry* **275**:37718-37724). The activity has been shown to be dependent on the presence of a synaptojanin-homologous region close to the C-terminus of the protein (Marcus *et al* (2001) *FEBS letters* **494**:201-207). The homologous protein IpgD also stimulates the activation of Akt in these cells (Marcus *et al* (2001)). The potential to activate Akt offers a number of therapeutic opportunities as it is a key regulator of cellular survival (reviewed in Vanhaesebroeck and Alessi (2000) *Biochemical Journal* **346**:561-576).

Inhibition of mitogen-activated protein kinase kinase. YopJ from *Yersinia pestis* is another translocated effector with a wide range of homologs including AvrA from *Salmonella* spp. and a variety of effectors from plant pathogens. YopJ has been shown to inactivate a broad range of mitogen-activated protein kinase kinases (MKKs) (Orth *et al* (1999) *Science* **285**:1920-1923) causing apoptosis in macrophages. YopJ is suggested to act as a ubiquitin-like protein protease causing increased turnover of signalling molecules via removal of a Sumo-1 tag from the MKK (Orth *et al* (2000) *Science* **290**:1594-1597). Interestingly in cell models of cytokine production and macrophage killing AvrA shows no activity despite its homology to YopJ suggesting that the specificity of the proteins may be different (Schesser K *et al* (2000) *Microbial Pathogenesis* **28**:59-70). In neuronal cells these different specificities may offer potential therapeutic applications for modulating MKKs involved in apoptosis or inflammatory responses.

Modulators of cellular trafficking. SpiC from *Salmonella enterica* inhibits the fusion of endosomal vesicles to prevent the exposure of *Salmonella* to lysosomal degradation (Uchiya *et al* (1999) *EMBO Journal* **18**:3924-3933). The ability to modulate intracellular trafficking pathways offers a number of therapeutic opportunities for modulating cycling of receptors or release of material from membrane bound vesicles.

A number of additional effector proteins are implicated in regulating and maintaining the intracellular compartments occupied by bacterial pathogens. *Salmonella*, in common with many other pathogens, establishes a specialised intracellular compartments. *Salmonella* has a dedicated type III secretion system that secretes proteins into the host cell cytosol from within this

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compartiment and the effectors secreted by this system (including SpiC, SopE/E2, SseE,F,G,J, PipA,B, SifA,B) maintain the integrity of this compartment. A recent paper described the synergistic effects of SseJ and SifA in regulating processes from the vacuolar membrane (Ruiz-Albert *et al* (2002) *Molecular microbiology* **44**;p645-661). These proteins and their counterparts from other intracellular pathogens have significant potential for treating disorders affecting intracellular trafficking pathways. RalF and a number of the other effectors described previously may also have significant therapeutic potential for such disorders.

The botulinum neurotoxins are a family of seven structurally similar, yet antigenically different, protein toxins whose primary site of action is the neuromuscular junction where they block the release of the transmitter acetylcholine. The action of these toxins on the peripheral nervous system of man and animals results in the syndrome botulism, which is characterised by widespread flaccid muscular paralysis (Shone (1986) in 'Natural Toxicants in Foods', Editor D. Watson, Ellis Harwood, UK). Each of the botulinum neurotoxins consist of two disulphide-linked subunits; a 100 kDa heavy subunit which plays a role in the initial binding and internalisation of the neurotoxin into the nerve ending (Dolly *et. al.* (1984) *Nature*, 307, 457-460) and a 50 kDa light subunit which acts intracellularly to block the exocytosis process (McInnes and Dolly (1990) *Febs Lett.*, 261, 323-326; de Paiva and Dolly (1990) *Febs Lett.*, 277, 171-174). Thus it is the heavy chains of the botulinum neurotoxins that impart their remarkable neuronal specificity.

Tetanus toxin is structurally very similar to botulinum neurotoxins but its primary site of action is the central nervous system where it blocks the release of inhibitory neurotransmitters from central synapses (Renshaw cells). As described for the botulinum toxins above, it is domains within the heavy chain of tetanus toxin that bind to receptors on neuronal cells.

The binding and internalisation (translocation) functions of the clostridial neurotoxin (tetanus and botulinum) heavy chains can be assigned to at least two domains within their structures. The initial binding step is energy-independent and appears to be mediated by one or more domains within the H_C fragment of the neurotoxin (C-terminal fragment of approximately 50kDa) (Shone *et al.* (1985), *Eur. J. Biochem.*, 151, 75-82) while the translocation step

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is energy-dependent and appears to be mediated by one or more domains within the H_N fragment of the neurotoxin (N-terminal fragment of approximately 50kDa).

5 Isolated heavy chains are non-toxic compared to the native neurotoxins and yet retain the high affinity binding for neuronal cells. Tetanus and the botulinum neurotoxins from most of the seven serotypes, together with their derived heavy chains, have been shown to bind a wide variety of neuronal cell types with high affinities in the nM range (e.g botulinum type B neurotoxin; Evans *et al.* (1986) Eur. J. Biochem. 154, 409-416). Another key characteristic of the binding of the tetanus and botulinum heavy chains to neuronal cells is that the receptor ligand recognised by the various toxin serotypes differ. Thus for example, botulinum type A heavy chain binds to a different receptor to botulinum type F heavy chain and these two ligands are non-competitive with respect to their binding to neuronal cells (Wadsworth *et al.* (1990), Biochem J. 268, 123-128). Of the clostridial neurotoxin serotypes so far characterised (tetanus, botulinum A, B, C₁, D, E and F), all appear to recognise distinct receptor populations on neuronal cells. Collectively, the clostridial neurotoxin heavy chains provide high affinity binding ligands that recognise a whole family of receptors that are specific to neuronal cells.

The present invention also provides constructs for the delivery of type III effector proteins specifically to neuronal cells. The mechanism by which the type III effector protein is delivered to the cell by these constructs is completely different to that used by the host bacteria. Instead of being injected directly into the cellular cytosol, specific constructs of the invention deliver the type III effector protein to cells via a number of sequentially acting biologically active domains and by a process resembling receptor-mediated endocytosis. Surprisingly, when delivered by this completely different mechanism, the type III effector proteins are biologically active within the cellular cytosol.

Particular constructs of the invention comprise three functional domains defined by their biological activities. These are:

- the type III effector moiety (for examples see Table1);
- a targeting domain that binds the construct to receptors and that provides a high degree of specificity to neuronal cells; and
- a translocation domain that after internalisation of the construct, effects

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the translocation of the type III effector moiety through the endosomal membrane into the cell cytosol.

5 The type III effector-containing construct may also contain 'linker proteins' by which these domains are interconnected. In one embodiment of the invention the type III effector moiety is linked to the translocation domain via a disulphide bridge.

10 In a preferred embodiment of the invention, the targeting domain is derived from a clostridial neurotoxin binding fragment (H_c domain). This may be derived from tetanus toxin or any one of the eight botulinum toxin serotypes (A-G). Delivery via the clostridial neurotoxin receptors differs significantly to the normal delivery route of the type III effectors and offers a number of advantages:

15 The clostridial H_c fragments bind with high affinity to receptors on the cell surface and provide high specificity to neuronal cells. The clostridial neurotoxins are internalised via an acidic endosome which triggers the translocation of the type III effector moiety across the membrane and into the cytosol.

20 For non-neuronal cells a wide range of high affinity binding domains have been defined for specific cell types. Examples are described for a number of cellular targets.

25 The agent can comprise a ligand or targeting domain, which binds to an endocrine cell and is thus rendered specific for these cell types. Examples of suitable ligands include iodine; thyroid stimulating hormone (TSH); TSH receptor antibodies; antibodies to the islet-specific monosialo-ganglioside GM2-1; insulin, insulin-like growth factor and antibodies to the receptors of both; TSH releasing hormone (protirelin) and antibodies to its receptor; FSH/LH releasing hormone (gonadorelin) and antibodies to its receptor; corticotrophin releasing hormone (CRH) and antibodies to its receptor; and ACTH and antibodies to its receptor.

35 Ligands suitable to target an agent to inflammatory cells include (i) for mast cells, complement receptors in general, including C4 domain of the Fc IgE, and antibodies/ligands to the C3a/C4a-R complement receptor; (ii) for eosinophils,

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antibodies/ligands to the C3a/C4a-R complement receptor, anti VLA-4 monoclonal antibody, anti-IL5 receptor, antigens or antibodies reactive toward CR4 complement receptor; (iii) for macrophages and monocytes, macrophage stimulating factor, (iv) for macrophages, monocytes and neutrophils, bacterial LPS and yeast B-glucans which bind to CR3, (v) for neutrophils, antibody to OX42, an antigen associated with the iC3b complement receptor, or IL8; (vi) for fibroblasts, mannose 6-phosphate/insulin-like growth factor-beta (M6P/IGF-II) receptor and PA2.26, antibody to a cell-surface receptor for active fibroblasts in mice.

Ligands suitable to target an agent to exocrine cells include pituitary adenyl cyclase activating peptide (PACAP-38) or an antibody to its receptor.

Ligands suitable to target an agent to immunological cells include Epstein Barr virus fragment/surface feature or idiotypic antibody (binds to CR2 receptor on B-lymphocytes and lymph node follicular dendritic cells).

Suitable ligands for targeting platelets for the treatment of disease states involving inappropriate platelet activation and thrombus formation include thrombin and TRAP (thrombin receptor agonist peptide) or antibodies to CD31/PECAM-1, CD24 or CD106/VCAM-1, and ligands for targeting cardiovascular endothelial cells for the treatment of hypertension include GP1b surface antigen recognising antibodies.

Suitable ligands for targeting osteoblasts for the treatment of a disease selected from osteopetrosis and osteoporosis include calcitonin, and for targeting an agent to osteoclasts include osteoclast differentiation factors (eg. TRANCE, or RANKL or OPGL), and an antibody to the receptor RANK.

In one embodiment of the invention the translocation domain is derived from a bacterial toxin. Examples of suitable translocation domains are those derived from the clostridial neurotoxins or diphtheria toxin.

In another embodiment of the invention, the translocation domain is a membrane disrupting or 'fusogenic' peptide, which functions as a translocation domain. An example of such a peptide is that derived from influenza virus haemagglutinin HA2 (residues 1-23).

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In one example of the construct of the invention, the type III effector protein is SigD from *Salmonella spp.* In another example of the construct of the invention, the type III effector protein is YopE from *Yersinia spp.*

5 In an example of the construct of the invention in which the type III effector moiety is SigD from *Salmonella spp.*, the construct may consist of the following:-
the SigD type III effector moiety;
the translocation domain from diphtheria toxin;
the binding domain (H_c domain) from botulinum type A neurotoxin; and
10 a linker peptide to enable attachment of the SigD effector to the translocation domain via a disulphide bridge.

In an another example of the construct of the invention in which the type III effector moiety is SigD from *Salmonella spp.*, the construct consists of the
15 following:-
the SigD type III effector moiety;
the translocation domain in the form of a fusogenic peptide;
the binding domain (H_c domain) from botulinum type F neurotoxin; and
a linker peptide to enable attachment of the SigD effector to the
20 translocation domain via a disulphide bridge.

In an example of the construct of the invention in which the type III effector moiety is YopE from *Yersinia spp.*, the construct may consist of the following:-
the YopE type III effector moiety;
25 the translocation domain from diphtheria toxin;
the binding domain (H_c domain) from botulinum type F neurotoxin; and
a linker peptide to enable attachment of the YopE effector to the translocation domain via a disulphide bridge.

30 The invention enables manipulation of cell signalling, and in a specific example SigD is incorporated into a construct of the invention and can be used to promote neuronal cell survival under stress. By targeting the appropriate intracellular signalling pathway, it is possible to simultaneously regulate a number of pathways to improve the prospects for neuronal survival. SigD (also
35 known as SopB) activates the protein kinase Akt, which is a key intermediate in the pro-survival signalling pathways mediated by various growth factors. Not only does Akt up-regulate pro-survival transcription factors such as NF- κ B,

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but it also down-regulates several pro-apoptotic factors such as Bad and Forkhead.

5 A number of type III and IV effectors function to maintain the intracellular niche of the bacteria within the host cell. Whilst some bacterial pathogens are released into the cell cytosol, many form and maintain a specialised intracellular compartment sometimes termed a vacuole. One of the principle functions of many effector protein is to regulate the fusion of the compartment with other intracellular compartments such as potentially damaging phagolysosomal. At the same time the pathogen may need to promote fusion with other membrane bound compartments, including recycling endosomes, to either provide nutrients to the encapsulated pathogen or allow the dissemination of the pathogen to other locations. Intracellular pathogens offer a wide range of effector molecules for regulating intracellular trafficking and membrane fusion.

15 The mechanism underlying the fusion of membrane bound vesicles is conserved in a number of cellular processes. Broadly speaking, membrane fusion events are classified either as secretory processes for the release of material from the plasma membrane, or as endocytic processes that move material from the plasma membrane to the lysosomal system. This simplified classification does not take into account retrograde and anterograde processes, which occur within these pathways, or multiple points of communication between the two pathways. The underlying mechanism in all membrane fusion events can be broken down into 4 component phases:

20 The transported material is concentrated at a specific site on the donor membrane and is "pinched off" in a vesicle that becomes separated from this membrane.

30 The vesicle is transported to the acceptor membrane along cytoskeletal fibres (e.g. microtubules).

35 The vesicle then attaches to the acceptor membrane via a "docking/tethering" mechanism mediated by SNARE complex proteins.

The vesicle and the acceptor membrane fuse to release the contents of the

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vesicle through the acceptor membrane.

Thus similar SNARE proteins and regulatory proteins underpin the fusion of endosomal vesicles with the lysosome, endoplasmic reticulum with the Golgi and trans-Golgi network, and secretory vesicles with the plasma membrane. The functional conservation of the membrane fusion mechanism means that a bacterial effector protein that would normally regulate the fusion of a specific event can be directed to modulate other fusion events. For example, an effector that blocks endosomal fusion with the lysosome can be redirected to block the fusion of secretory vesicles with the plasma membrane, or ER vesicles with the Golgi network.

One of the key classes of regulatory proteins that have been defined in vesicle trafficking are small GTPases of the Ras superfamily termed Rab proteins (or Ypt proteins in yeast). Rab proteins are implicated in every stage of membrane fusion. For example Rab 1,2,5 and 9 are involved in sorting material for transport (stage 1 above), Rab5,6,27 and Sec4 mediate transport (stage 2), Rab1,5, Ypt1,7 Sec4 influence docking to the acceptor membrane (stage 3) and other Rab proteins implicated in promoting membrane fusion. The list above shows that certain Rab proteins, such as Rab1 and Rab5, are involved in more than 1 stage of the fusion process. Similarly some Rab proteins are present on all membrane vesicles whilst others have more specialised roles in specific fusion events.

Rab proteins are key potential targets for modification by either bacterial pathogens intent on blocking or promoting membrane fusion events or by therapeutic agents designed to regulate intracellular trafficking. One of the first effector proteins to be described as having an effect on Rab function was the secreted effector protein SopE2 from *Salmonella* species. SopE2 acts as a guanine nucleotide exchange factor for Rab5a resulting in increased activation of the protein on the cell membrane. This activity has been correlated with increased survival of *Salmonella* in infected HeLa cells and macrophages (Cell Microbiol. 3 p473). SpiC is another *Salmonella* effector that blocks endosome fusion (EMBO J. 18p3924-3933). Unlike SopE, which shows some conservation with normal cellular regulators of GTPase, SpiC shows no clear homology to other proteins. Its ability to block one of the four stages of vesicle fusion is known. It could exert its activity at the level of the SNARE proteins,

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modulate Rab function directly or operate at the level of one of the regulators of Rab function. Membrane insertion is essential for Rab activity. Rab proteins form a stable complex with Rab escort protein (REP) in the cytosol and this is a substrate for a geranyl geranyl transferase (RabGGT) which adds a C-terminal isoprenoid moiety. In the absence of REP or RabGGT the Rab protein would remain in an inactive form in the cytosol. REP also mediates the membrane insertion of the modified Rab into the donor membrane. Rab proteins can also be retrieved from the membrane via the action of Rab GDP dissociation inhibitor (RabGDI). All of these proteins are potential targets for bacterial pathogens to alter membrane fusion events. The precise effect would depend on whether alterations cause an increase or decrease in the levels of active Rab in the donor membrane, and the specificity for particular Rab proteins.

A number of human diseases have now been identified in which mutations affect either Rab proteins or their regulators. These human diseases serve to illustrate the cellular effects of alterations in Rab control in cells. Thus mutations in Rab27 (Griscelli syndrome), REP1 (choroideroma), RabGDI α (X-linked mental retardation) and RabGGT α subunit (Hermansky-Pudlak syndrome) are all implicated in human disease (as reviewed in Seabra *et al Trends in Molecular Medicine* (2002) 8;23-26, Olkkonen and Ikonen *New England Journal of Medicine* (2000) 343;1104)). A wide range of human diseases involve defects in intracellular trafficking (as reviewed in Aridor and Hannan *Traffic* (2000) 1;836-851). Modulation of membrane fusion via the specialised properties of bacterial effector proteins directed at one of the 4 mechanisms described above offers therapeutic opportunities for these diseases and others where transport properties are affected.

The targeting of the membrane fusion event between secretory vesicles and the plasma membrane allow the control of secretion from cells. Effectors that alter regulation of specific Rab proteins, either directly or via one of the mechanisms described above, including Rab3a,b,c and d, Rab8a and b, Rab26, Rab27a Rab37, or affect any of the other molecular events of membrane fusion (1-4 described above) can regulate secretion. Effector proteins can be applied to either increase or decrease secretion from a specific cell type. In a therapeutic context this is valuable for the treatment of a wide range of disorders including muscle spasms (blepharospasm, torticollis etc)

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hypersecretion disorders (COPD, bronchitis, asthma).

By modulating the fusion of recycling endosomes with either the lysosome or the plasma membrane it also possible to modulate the presentation of specific families of cell surface marker. Again effectors directed to alter regulation of specific Rab proteins, such as Rab4a and b, Rab11a and b, Rab15, Rab17, Rab18 or affect other molecular events in the fusion mechanism, can either up or down regulate presentation of cell surface marker. Therapeutically this has enormous potential for altering the response of cells to external stimuli (e.g. modulating response to growth factors, hormones, cytokines, chemokines or other signalling molecules), modifying the recognition of cells by external factors (e.g. immune surveillance) or for switching cell signalling pathways on or off.

Using constructs of the invention, therapeutic intervention can be provided in neurodegenerative disorders such as Alzheimer's disease and Prion diseases (vCJD). Both diseases are characterised by the accumulation of insoluble protein plaques due to misfolding of cellular proteins. In both cases an intracellular amplification of misfolded protein, via passage through endosomal-lysosomal compartments, is implicated in the progression of the disease. Neuronally targeted bacterial effectors as described herein, which modulate the fusion of endosomal and lysosomal compartments, allow control of the accumulation of insoluble protein. As this is one of the key survival strategies of many intracellular bacterial pathogens, a number of therapeutic molecules are available, for example Salmonella effectors such as SpiC, SptP and SopE2.

In still further embodiments of the invention, constructs are provided for inhibition or promotion of secretion, containing a type III effector and a targetting moiety. Specific effectors for this purpose are selected from SpiC, SopE, RalF, Sse E, F, G and J, PipA, PipB, SifA and SifB. These constructs target the membrane fusion event between secretory vesicles and the plasma membrane to allow the control of secretion from cells. Effectors that alter regulation of specific Rab proteins, either directly or via one of the mechanisms described above, including Rab3a,b,c and d, Rab8a and b, Rab26, Rab27a Rab37, or affect any of the other molecular events of membrane fusion, can regulate secretion. Effector proteins can be applied to either increase or

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decrease secretion from a specific cell type. In a therapeutic context this is valuable for the treatment of a wide range of disorders including muscle spasms (blepharospasm, torticollis etc) hypersecretion disorders (COPD, bronchitis, asthma).

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The pathogenic strategy to establish a specialised intracellular niche and to modulate fusion of that compartment with other vesicles is conserved for a vast range of pathogens. Not only does this provide a vast range of molecules capable of modulating the cellular events as described above, but it also provides an array of potential therapeutic targets for such molecules. Although many of the intracellular pathogens described in table 2 establish membrane bound compartments, the precise biochemistry and the signalling events and effectors needed to maintain these compartments are very different. A few intracellular pathogens escape from the phagosomal or endosomal compartment in which they enter the cell. The effector proteins involved in this process are incompatible with the life cycle of pathogens that remain in membrane compartments. The effector proteins of two intracellular pathogens existing in membrane bound vesicles are also not necessarily compatible. For example, enhancement of Rab5a activity by *Salmonella* in macrophages is correlated with enhanced survival (Cell Microbiology 3;473-). However, increases in Rab5a expression/activity accelerates intracellular destruction of *Listeria monocytogenes* in macrophages (J. Biological Chemistry 274;11459). The *Salmonella* effector proteins that are likely to be involved in Rab5a recruitment (e.g. SopE2, SpiC or other SPI-2 secreted effectors) are therefore potential therapeutic agents for treating intracellular *Listeria*.

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In its crudest form anti-microbial therapy could involve treating one intracellular pathogen with a second pathogen on the basis that the two intracellular compartments and requirements of the organisms would not be compatible. For example treatment of TB infected macrophages with *Salmonella* might be expected to result in provoked "vacuole" lysosome fusion within the macrophage leading to the eradication of the TB. The type and fate of the super-infecting pathogen would have to be carefully chosen so as not to exacerbate the infectivity or spread of the original organism.

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A refinement of the superinfection strategy would therefore focus on the targeted delivery of effector molecules to specific target cells as described by

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5 this invention. This could either utilise a highly attenuated pathogen (e.g. *Salmonella* that only secretes SopE2 or SptP) or targeted protein delivery (e.g. using a toxin delivery domain, antibody or similar cell targeting ligands). Protective antigen from *Bacillus anthracis* would be capable of targeting effectors to macrophages for the treatment of a wide range of bacterial pathogens. The specific addition of carbohydrate moieties will enable specific targeting of pools of macrophages via the mannose receptor (e.g. Vyas et al, International Journal of Pharmaceutics (2000) 210p1-14). A cell surface marker specific for infected cells (as distinct from uninfected cells) would offer an ideal target for delivery systems. The cell type infected by the pathogen would determine the choice of delivery ligand whilst the precise fate of the cell compartment would determine the choice of effector (e.g. cell apoptosis, lysis, endosome-lysosome fusion, endosome acidification etc).

15 A key benefit of this type of therapy is that the effector proteins are not intrinsically toxic to the cell and therefore delivery of the protein to uninfected target cells is unlikely to have any deleterious effects. In this case, whilst desirable, the precise specificity of the targeting ligand is not essential for successful therapy.

20 The wide range of intracellular pathogens and the difficulty in treating/immunising against these organisms make this approach a valuable alternative to antibiotic therapy. The method is also attractive as avoidance of the antimicrobial agent either means that the pathogen must produce a molecule capable of overriding the effector-induced cell stimulus or must significantly modify its lifestyle. For obligate intracellular pathogens or where the intracellular stage is essential for propagation, this may offer greater hopes for extended antimicrobial use than current antibiotic strategies targeted at specific biochemical interactions.

30 In another example of the invention in which the effector protein is SpiC from *Salmonella* spp, the construct may consist of the following:-

the SpiC effector moiety fused to a domain capable of interacting with protective antigen;

35 the protective antigen from *Bacillus anthracis*;

where the construct is either co-administered or where the SpiC moiety is administered after the protective antigen.

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The constructs of the invention are preferably produced either wholly or partially by recombinant technology. In an embodiment of the invention where a construct of the invention is produced by recombinant technology, the construct of the invention will be produced as a single multi-domain polypeptide comprising from the N-terminus:-

- the type III effector moiety;
- a linker peptide;
- the translocation domain; and
- the binding domain.

In such a construct, the C-terminus of the type III effector protein is fused to the N-terminus of the translocation domain via the linker peptide. An example of such a linker peptide is the sequence CGLVPAGSGP which contains the thrombin protease cleavage site and a cysteine residue for disulphide bridge formation. The latter single chain fusion protein may then be treated with thrombin to give a dichain protein in which the type III effector is linked to the translocation domain by a disulphide link. In another example of a linker peptide in which the translocation domain does not contain a free cysteine residue near its C-terminus, such as is the case when the translocation domain is a fusogenic peptide, the linker peptide contains both cysteine residues required for the disulphide bridge. An example of the latter linker peptide is the amino acid sequence: CGLVPAGSGPSAGSSAC.

In an example of the construct of the invention in which the type III effector moiety is SigD from *Salmonella spp* produced by recombinant technology, the construct may consist of polypeptide containing (from the N-terminus) the following domains:-

- the SigD type III effector moiety;
- linker peptide (sequence CGLVPAGSGP) to enable attachment of the SigD effector to the translocation domain via a disulphide bridge;
- the translocation domain from diphtheria toxin (residues 194-386); and
- the binding domain (H_c domain) from botulinum type A neurotoxin (residues 872-1296).

The constructs of the invention may also be produced using chemical cross-linking methods. Various strategies are known by which type III effector

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proteins can be linked to a polypeptide consisting of the translocation domain and binding domain using a variety of established chemical cross-linking techniques. Using these techniques a variety of type III effector constructs can be produced. The type III effector protein is, for example, derivatised with the cross-linking reagent N-succinimidyl 3-[2-pyridyldithio] propionate. The derivatised type III effector is then linked to a peptide containing a translocation domain and binding domain via a free cysteine residue present on the translocation domain.

Protein effectors can be altered to allow their delivery to intracellular compartments other than their usual site of action. For example, mitochondrial or nuclear targeting signals could be added to direct the effector to these compartments. By covalently linking the effector to the targeting domain the effector can be retained in the endosome/lysosome compartment, which would not normally be accessible by bacterial delivery. Effectors can be targeted to specific membrane locations via lipid modifications including myristoylation, palmitoylation, or the addition of short proteins domains that might include SH2, SH3, WW domains, fragments of Rab proteins or synaptojanin-like domains. Those practised in the art would recognise that these targeting strategies offer an advantage for certain therapeutic strategies.

Constructs of the invention may be introduced into either neuronal or non-neuronal tissue using methods known in the art. By subsequent specific binding to neuronal cell tissue, the targeted construct exerts its therapeutic effects. Ideally, the construct is injected near a site requiring therapeutic intervention.

The construct of the invention may be produced as a suspension, emulsion, solution or as a freeze dried powder depending on the application and properties of the therapeutic substance. The construct of the invention may be resuspended or diluted in a variety of pharmaceutically acceptable liquids depending on the application.

"Clostridial neurotoxin" means either tetanus neurotoxin or one of the seven botulinum neurotoxins, the latter being designated as serotypes A, B C₁, D, E, F or G, and reference to the domain of a toxin is intended as a reference to the intact domain or to a fragment or derivative thereof which retains the essential function of the domain.

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"Conjugate" means, in relation to two polypeptides, that the polypeptides are linked by a covalent bond, typically forming a single polypeptide as a result, or by a di-sulphide bond.

5 "Binding domain" means a polypeptide which displays high affinity binding specific to a target cell, e.g. neuronal cell binding corresponding to that of a clostridial neurotoxin. Examples of binding domains derived from clostridial neurotoxins are as follows:-

10	Botulinum type A neurotoxin	– amino acid residues (872 - 1296)
	Botulinum type B neurotoxin	– amino acid residues (859 - 1291)
	Botulinum type C neurotoxin	– amino acid residues (867 - 1291)
	Botulinum type D neurotoxin	– amino acid residues (863 - 1276)
	Botulinum type E neurotoxin	– amino acid residues (846 - 1252)
15	Botulinum type F neurotoxin	– amino acid residues (865 - 1278)
	Botulinum type G neurotoxin	– amino acid residues (864 - 1297)
	Tetanus neurotoxin	– amino acid residues (880 - 1315)

20 "High affinity binding specific to neuronal cell corresponding to that of a clostridial neurotoxin" refers to the ability of a ligand to bind strongly to cell surface receptors of neuronal cells that are involved in specific binding of a given neurotoxin. The capacity of a given ligand to bind strongly to these cell surface receptors may be assessed using conventional competitive binding assays. In such assays radiolabelled clostridial neurotoxin is contacted with
 25 neuronal cells in the presence of various concentrations of non-radiolabelled ligands. The ligand mixture is incubated with the cells, at low temperature (0-3°C) to prevent ligand internalization, during which competition between the radiolabelled clostridial neurotoxin and non-labelled ligand may occur. In such assays when the unlabelled ligand used is the same as that of the labelled
 30 neurotoxin, the radiolabelled clostridial neurotoxin will be displaced from the neuronal cell receptors as the concentration of non-labelled neurotoxin is increased. The competition curve obtained in this case will therefore be representative of the behaviour of a ligand which shows "high affinity binding specificity to neuronal cells corresponding to that of a clostridial neurotoxin", as
 35 used herein.

A carrier that "targets" a particular cell generally does so due to binding of the

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carrier, or a portion thereof, to that cell and, by way of example, many different ligands with given cell type specificity are described herein.

"Translocation domain" means a domain or fragment of a protein which effects transport of itself and/or other proteins and substances across a membrane or lipid bilayer. The latter membrane may be that of an endosome where translocation will occur during the process of receptor-mediated endocytosis. Translocation domains can frequently be identified by the property of being able to form measurable pores in lipid membranes at low pH (Shone *et al.* Eur J. Biochem. 167, 175-180). Examples of translocation domains are set out in more detail below:

Diphtheria toxin	– amino acid residues (194 - 386)
Botulinum type A neurotoxin	– amino acid residues (449 - 871)
Botulinum type B neurotoxin	– amino acid residues (441 - 858)
Botulinum type C neurotoxin	– amino acid residues (442 - 866)
Botulinum type D neurotoxin	– amino acid residues (446 - 862)
Botulinum type E neurotoxin	– amino acid residues (423 - 845)
Botulinum type F neurotoxin	– amino acid residues (440 - 864)
Botulinum type G neurotoxin	– amino acid residues (442 - 863)
Tetanus neurotoxin	– amino acid residues (458 - 879)

Translocation domains are frequently referred to herein as "H_N domains".

"Translocation" in relation to translocation domain, means the internalization events that occur after binding to the cell surface. These events lead to the transport of substances into the cytosol of target cells.

"Injected effector secreted by type III or type IV secretion system" means bacterial proteins that are injected into host cells (mammalian, plant, insect, fish or other) via a modified pilus or "needle-like" injection system frequently referred to as type III or type IV secretion systems" and the term embraces fragments, modifications and variations thereof that retain the essential effector activity.

The invention thus uses modification of intracellular signalling for promoting neuronal growth. Many of the effectors and inhibitors that control the

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development of the growth cone act through common intracellular signalling pathways that modulate the phosphorylation state of cytoskeletal components and that ultimately determine whether the axon grows or collapses. The appropriate manipulation of intracellular signalling is therefore a powerful approach for eliminating the need for multiple inhibitors of the many factors shown to induce apoptosis and growth cone collapse. The up-regulation of transcription factors that inhibit apoptosis is an example of manipulation of intracellular signalling to promote neural regeneration.

Strategies for therapeutic intervention using the effectors and compositions of the invention include the delivery of agents to eliminate stress-inducing factors and the modification of intracellular signalling to promote cell survival. The latter approach is particularly powerful and the present invention describes conjugates with type III effector moieties which allow such strategies to be pursued.

The constructs of this invention use a specific targeting system to ensure delivery of the therapeutic agent to the desired cells and uses bacterial toxins that have evolved to regulate key stages in the cell signalling machinery of the cells. This strategy offers a number of advantages over other drug platforms. The cell specificity ensures that any alterations in cell signalling occur only in the cells where this modification is desirable and not in other adjacent cells. For example, in neuronal cell-targeted constructs, changes in signalling would only take place in neurones and not in adjacent glial cells where such changes might not be desirable. By targeting key intermediates in the signalling pathway it is possible to co-ordinately regulate a number of overlapping cellular events to promote the desired effect. For example, the activation of Akt by SigD causes an effect on cells by co-ordinating a number of signalling pathways to actively promote cell survival and block the induction of apoptosis in response to stress factors. This is also a good example of an effector that activates a component of a cell-signalling pathway. Most drug discovery approaches tend to identify inhibitors of specific components.

The invention is now illustrated in the following specific examples.

Examples:

Example 1. Cloning and expression of type III effector genes.

Standard molecular biology protocols were used for all genetic manipulations (Sambrook *et al* 1989, Molecular cloning; A laboratory manual. Second Edition, Cold Spring Harbor Laboratory Press, New York.). Genes encoding Type III effectors, truncated versions removing the N-terminal hydrophobic domain (e.g removal of amino acids 1-28 for SigD, 1-69 for SptP, 1-76 for SopE), or individual sub-domains (e.g. ExoS GAP domain amino acids 96-234 and ADP-ribosyltransferase domain amino acids 232-453), were amplified from genomic DNA by PCR to generate suitable restriction sites for cloning. In some cases synthetic genes were prepared with codon usage optimised for expression in *E.coli*. Restriction enzymes such as *Bam*HI (5') and *Bgl*II (3') were used for cloning with reading frames maintained. Constructs were sequenced to confirm the presence of the correct sequence. Constructs for expression were subcloned, as a suitable fragment, into an expression vector carrying a T7 polymerase promoter site (e.g. pET28, pET30 or derivatives (Novagen Inc, Madison, WI)), to generate a fusion with maltose binding protein (e.g. pMALc2x (NEB)) or into other expression vectors known to those familiar with the art. Clones with confirmed sequences were used to transform expression hosts: For T7 polymerase vectors *E.coli* BL21 (DE3) (Studier and Moffatt 1986 *Journal of Molecular Biology* 189:113-130) JM109 (DE3) or equivalent strains with a DE3 lysogen. For pMALc2x JM109, BL21, TG1, TB1 or other suitable expression strains.

In addition to the expression of type III effectors as standard fusion proteins an additional approach was used to generate fusion proteins. The type III effector or truncated effector generated as above were cloned into the 5' end of a gene encoding a cell targeting ligand, which include toxin fragments, antibodies, growth factors, lectins, interleukins, peptides. These fusion proteins were cloned and expressed as either 6-His tagged, MBP tagged or other fusions as described above.

Expression cultures were grown in Terrific Broth containing 30µg/ml kanamycin and 0.5% (w/v) glucose to an OD₆₀₀ of 2.0 and protein expression was induced with 500µM IPTG for 2 hours. Cells were lysed by either sonication or suitable detergent treatment (e.g. Bugbuster reagent; Novagen), cell debris pelleted by centrifugation and the supernatant loaded onto a metal chelate column charged

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with Cu²⁺ (Amersham-Pharmacia Biotech, Uppsala, Sweden).

The recombinant proteins expressed from pET vectors contain amino-terminal histidine (6-His) and T7 peptide tags allowing proteins to be purified by affinity chromatography on either a Cu²⁺ charged metal chelate column. After loading proteins on the column and washing, proteins were eluted using imidazole. All buffers were used as specified by manufacturers. Where appropriate removal of the purification tag was carried out according to manufacturers instructions.

MBP fusions were purified on amylose resin columns as described by the manufacturer (NEB) following growth in Terrific Broth containing 100 µg/ml ampicillin and lysis as described above.

Other fusion systems were used according to manufacturer's instructions and purification carried out on suitable columns using defined methods.

Example 2. Production of recombinant targeting vectors consisting of translocation and binding domains

Standard molecular biology protocols were used for all genetic manipulations (Sambrook *et al* 1989, Molecular cloning; A laboratory manual. Second Edition, Cold Spring Harbor Laboratory Press, New York.) Clostridial neurotoxin binding domains (BoNT/Hc or TeNT/Hc) derived from either their native genes or synthetic genes with codon usage optimised for expression in *E.coli* were amplified by PCR. Introduced *Bam*HI (5') restriction sites and *Hind*III, *Sal*I or *Eco*RI (3') sites were used for most cloning operations with reading frames designed to start with the first base of the restriction site. Constructs were sequenced to confirm the presence of the correct sequence. The translocation domain of diphtheria toxin (DipT) was amplified from its native gene to introduce *Bam*HI and *Bgl*II sites at the 5' and 3' ends respectively. This *Bam*HI and *Bgl*II fragment was subcloned into the *Bam*HI site at the 5' end of the Hc fragment to generate an in-frame fusion. The entire heavy chain fragment (DipT-Hc) was excised as a *Bam*HI-*Hind*III or *Bam*HI-*Sal*I or *Bam*HI-*Eco*RI fragment and subcloned into a suitable expression vector.

Constructs for expression were subcloned into either an expression vector carrying a T7 polymerase promoter site (e.g. pET28, pET30 or derivatives

- 31 -

(Novagen Inc, Madison, WI)) or to generate a fusion with maltose binding protein (e.g. pMALc2x (NEB)) as a suitable fragment. Clones with confirmed sequences were used to transform expression hosts: For T7 polymerase vectors *E.coli* BL21 (DE3) (Studier and Moffatt 1986 *Journal of Molecular Biology* 189:113-130) JM109 (DE3) or equivalent strains with a DE3 lysogen. For pMalc2x JM109, BL21, TG1, TB1 or other suitable expression strains.

The recombinant proteins expressed from pET vectors contain amino-terminal histidine (6-His) and T7 peptide tags allowing proteins to be purified by affinity chromatography on either a Cu^{2+} charged metal chelate column. Expression cultures were grown in Terrific Broth containing 30microg/ml kanamycin and 0.5% (w/v) glucose to an OD_{600} of 2.0 and protein expression was induced with 500microM IPTG for 2 hours. Cells were lysed by either sonication or suitable detergent treatment (e.g. Bugbuster reagent; Novagen), cell debris pelleted by centrifugation and the supernatant loaded onto a metal chelate column charged with Cu^{2+} (Amersham-Pharmacia Biotech, Uppsala, Sweden). After loading proteins on the column and washing, proteins were eluted using imidazole. All buffers were used as specified by manufacturers. Where appropriate removal of the purification tag was carried out according to manufacturers instructions.

MBP fusions were purified on amylose resin columns as described by the manufacturer (NEB) following growth in Terrific Broth containing 100 microg/ml ampicillin and lysis as described above.

Thrombin or factor Xa protease sites were included within the protein for subsequent removal of these purification tags.

Additional sequences for adding affinity purification tags and one or more specific protease sites for the subsequent removal of these affinity tags may also be included in the reading frame of the gene products.

Other coding sequences that enable expression of the desired protein would also be acceptable. Other tags or linking sites may also be incorporated into the sequence.

Using the techniques described above, targeting vector fragments were constructed by fusing domains of the H_c fragments of either botulinum type A, type F or tetanus neurotoxins with the translocation domain of diphtheria toxin.

Example 3. Preparation of botulinum heavy chains by chemical methods.

5 The various serotypes of the clostridial neurotoxins may be prepared and purified from various toxigenic strains of *Clostridium botulinum* and *Clostridium tetani* by methods employing standard protein purification techniques as described previously (Shone and Tranter 1995, Current Topics in Microbiology, 194, 143-160; Springer). Samples of botulinum neurotoxin (1mg/ml) are dialysed against a buffer containing 50mM Tris-HCl pH 8.0, 1M NaCl and 2.5M
10 urea for at least 4 hours at 4°C and then made 100mM with dithiothreitol and incubated for 16h at 22°C. The cloudy solution, which contains precipitated light chain, is then centrifuged at 15000 x g for 2 minutes and the supernatant fluid containing the heavy chain retained and dialysed against 50mM HEPES pH 7.5 containing 0.2M NaCl and 5mM dithiothreitol for at least 4 hours at 4°C. The
15 dialysed heavy chain is centrifuged at 15000 x g for 2 minutes and the supernatant retained and dialysed thoroughly against 50mM HEPES pH 7.5 buffer containing 0.2M NaCl and stored at -70°C. The latter procedure yields heavy chain >95% pure with a free cysteine residue which can be used for chemical coupling purposes. Biological (binding) activity of the heavy chain
20 may be assayed as described in Example 5.

The heavy chains of the botulinum neurotoxins may also be produced by chromatography on QAE Sephadex as described by the methods in Shone and Tranter (1995) (Current Topics in Microbiology, 194, 143-160; Springer).

Example 4. Chemical conjugation of proteins

Recombinant SigD type III effector from *Salmonella spp.* was cloned and purified as described in Example 1. The SigD type III effector was chemically
30 modified by treatment with a 3-5 molar excess of N-succinimidyl 3-[2-pyridyldithio] propionate (SPDP) in 0.05M Hepes buffer pH 7.0 containing 0.1M NaCl for 60 min at 22°C. The excess SPDP was removed by dialysis against the same buffer at 4°C for 16h. The substituted SigD effector was then mixed in a 1:1 ratio and incubated at 4°C for 16h with a targeting vector comprising
35 a translocation domain (with an available free cysteine residue) and a neuronal targeting domain (see Example 2). The latter may also be native heavy chain purified from *Clostridium botulinum* type A neurotoxin purified as described in

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Example 3. During the incubation period the SigD effector was conjugated to the targeting vector fragment by a free sulphhydryl group. After incubation, the SigD-construct was purified by gel filtration chromatography on Sephadex G200.

5

Example 5. Assay of the biological activity of constructs - demonstration of high affinity binding to neuronal cells.

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Clostridial neurotoxins may be labelled with ¹²⁵-iodine using chloramine-T and its binding to various cells assessed by standard methods such as described in Evans *et al.* 1986, Eur J. Biochem., 154, 409 or Wadsworth *et al.* 1990, Biochem. J. 268, 123). In these experiments the ability of Type III constructs to compete with native clostridial neurotoxins for receptors present on neuronal cells or brain synaptosomes was assessed. All binding experiments were carried out in binding buffers. For the botulinum neurotoxins this buffer consisted of: 50mM HEPES pH 7.0, 30mM NaCl, 0.25% sucrose, 0.25% bovine serum albumin. For tetanus toxin, the binding buffer was: 0.05M tris-acetate pH 6.0 containing 0.6% bovine serum albumin. In a typical binding experiment the radiolabelled clostridial neurotoxin was held at a fixed concentration of between 1-20nM. Reaction mixtures were prepared by mixing the radiolabelled toxin with various concentrations of unlabelled neurotoxin or construct. The reaction mixtures were then added to neuronal cells or rat brain synaptosomes and then incubated at 0-3°C for 2hr. After this period the neuronal cells of synaptosomes were washed twice with binding ice-cold binding buffer and the amount of labelled clostridial neurotoxin bound to cells or synaptosomes was assessed by α -counting. In an experiment using an Type III effector construct what contained the binding domain from botulinum type A neurotoxin, the construct was found to compete with ¹²⁵I-labelled botulinum type A neurotoxin for neuronal cell receptors in a similar manner to unlabelled native botulinum type A neurotoxin. These data showed that the construct had retained binding properties of the native neurotoxin.

Example 6. Recombinant Type III effector constructs

35

Recombinant Type III effector-targeting vector constructs were prepared comprising a combination of the following elements:-
- a type III effector (e.g. SigD from *Salmonella* spp.)

- 34 -

- a linker region, which allows the formation of a disulphide bond between the type III effectors and the translocation domain and which also contains a unique protease cleavage site for cleavage by factor Xa or thrombin to allow the formation of a dichain molecule;

5

- a translocation domain from diphtheria toxin or a endosomolytic (fusogenic) peptide from influenza virus haemagglutinin); and

10

- a neuronal cell-specific binding domain (e.g. from tetanus or botulinum neurotoxin type A or botulinum neurotoxin type F).

The protein sequences of these various domains form specific embodiments of the invention and are shown below the examples.

15

To confirm the nature of their structure, the recombinant Type III effector-targeting vector constructs were converted to the dichain form by treatment with a unique protease corresponding to the cleavage site sequences within the linker region. Conjugates containing the thrombin cleavage site were treated with thrombin (20microg per mg of conjugate) for 20h at 37°C; conjugates containing the factor Xa cleavage site were treated with factor Xa (20microg per mg of conjugate) for 20 min at 22°C.

20

25

On SDS-PAGE gels, under non-reducing conditions, the majority of Type III effector-targeting vector construct appeared as single band. In the presence of reducing agent (dithiothreitol) two bands were observed corresponding to the type III effector and targeting vector (translocation and binding domains). These data illustrate that, after treatment with the unique protease, the conjugates consist of the latter two components which are linked by a disulphide bridge.

30

Example 7. Formation of Type III effector constructs from Type III effector-diphtheria toxin A (CRM197) fusion proteins.

Type III effector-targeting vector constructs may also formed *in vitro* by reconstitution from two recombinant fragments. These are:-

35

A Type III effector fused to inactive diphtheria fragment A (CRM197) as described in Example 1.

- 35 -

A recombinant targeting vector in which the translocation domain of diphtheria toxin is fused to a neuronal targeting domain such as that from a clostridial neurotoxin. Production of these is described in Example 2.

5 Type III effector constructs may be formed by mixing fragments 1 and 2 in equimolar proportions in the presence of 10mM dithiothreitol and then completely removing the reducing agent by dialysis against phosphate buffered saline at pH 7.4 followed by dialysis against HEPES (0.05M, pH 7.4) containing 0.15 M NaCl. As described above in Example 6, these constructs
10 appear as a single band in SDS gels under non-reducing conditions and two bands in the presence of a reducing agent.

Example 8. Formulation of the Type III effector construct for clinical use.

15 In a formulation of the Type III effector construct for clinical use, recombinant Type III effector construct would be prepared under current Good Manufacturing Procedures. The construct would be transferred, by dilution, to a solution to give the product stability during freeze-drying. Such a formulation
20 may contain Type III effector construct (concentration between 0.1 -10 mg/ml) in 5mM HEPES buffer (pH 7.2), 50mM NaCl, 1% lactose. The solution, after sterile filtration, would be aliquotted, freeze-dried and stored under nitrogen at -20°C.

Example 9. Production of constructs with neuroprotective properties.

25 SigD was cloned (without the first 29 condons) using the methods outlined in Example 1. The protein was expressed and purified either as a fusion with maltose binding protein (e.g. using pMALc2x) or with a Histidine6 (e.g. using pET28a). Purification tags were then removed by standard procedures after
30 affinity purification of the fusion protein. Chemical constructs of SigD were prepared as outlined in Example 4.

35 A recombinant construct of the invention containing SigD linked to the translocation domain and binding domain of botulinum type A neurotoxin was prepared as outlined in Example 6 using the standard molecular biology procedures outlined in Example 1.

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Application of the above constructs to neuronal cells leads to the receptor-mediated internalisation of SigD and subsequent activation of Akt Kinase. Such cells have an enhanced ability to withstand stress such as growth factor removal.

5

Example 10. Constructs for the treatment of neurodegenerative disease

10

Constructs for treatment of neurodegenerative disease and containing the effectors SpiC, SptP or SopE2 were prepared as outlined in Example 9.

Example 11. Constructs for regulating cellular secretion and expression of cell surface receptors

15

For neuronal cells, constructs containing the effectors SpiC, SopE, RalF, SseE,F,G and J, PipA and B, SifA and B were prepared as outlined in Example 9.

20

For non-neuronal cells, the targeting domain may be replaced by a ligand with specificity for the target cell type. Such ligands may be selected from a list including: antibodies, carbohydrates, vitamins, hormones, cytokines, lectins, interleukins, peptides, growth factors, cell attachment proteins, toxin fragments, viral coat proteins.

25

Example 12 Constructs for the treatment of intracellular pathogens

30

Constructs containing the effectors SopE/SopE2, RalF, SpiC, SseE,F,G or J, PipA or B, SifA or B, or other effectors, for example those described in table 1, are useful therapeutic agents for treatment of disease.

35

Constructs were prepared essentially as described in example 9 but with a suitable binding domain selected from a list including; antibodies, carbohydrates, vitamins, hormones, cytokines, lectins, interleukins, peptides, growth factors, cell attachment proteins, toxin fragments, viral coat proteins etc. For targeting to macrophages this might include protective antigen from *Bacillus anthracis* or a carbohydrate moiety such as a mannose modification allowing specific uptake.

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A recombinant construct of the invention includes an effector protein and a binding domain suitable for targeting the effector to a desired cell type.

5

When delivered to cells such constructs result in cellular events that cause the death of the intracellular pathogen, prevent its release from the infected cell type or otherwise reduce its ability to infect and cause disease.

10

Further embodiments of the invention are represented by all combinations of the recited effectors with the recited linker-translocation domain-binding domain conjugates.

15

The present application includes a sequence listing in which the following sequences referred to by their SEQ ID No.s represent the following embodiments of the invention:-

20

<u>SEQ ID. NO.</u>	<u>DESCRIPTION</u>
--------------------	--------------------

1	Diphtheria toxin translocation domain
---	---------------------------------------

2	Diphtheria toxin translocation domain, TeNT-Hc
---	--

3	Thrombin linker, Diphtheria toxin translocation domain, TeNT-Hc
---	---

25

4	Factor Xa linker, Diphtheria toxin translocation domain, TeNT-Hc
---	--

5	Diphtheria toxin translocation domain, BoNT/F-Hc
---	--

30

6	Thrombin linker, Diphtheria toxin translocation domain, BoNT/F-Hc
---	---

7	Factor Xa linker, Diphtheria toxin translocation domain, BoNT/F-Hc
---	--

35

8	AAC46234 invasion gene D protein [Salmonella typhimurium] SigD
---	--

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	9	AAF21057 invasion protein D [<i>Salmonella typhimurium</i>] SopB
5	10	CAC05808 IpgD, secreted by the Mxi-Spa machinery, modulates entry of bacteria into epithelial cells [<i>Shigella flexneri</i>]
10	11	AAC 69766 targeted effector protein [<i>Yersinia pestis</i>] YopJ
	12	AAC02071 SopE [<i>Salmonella typhimurium</i>]
15	13	AAC44349 protein tyrosine phosphatase SptP [<i>Salmonella typhimurium</i>]
	14	NP_047628 targeted effector [<i>Yersinia pestis</i>] YopE
	15	AAK39624 exoenzyme S [<i>Pseudomonas aeruginosa</i>]
20	16	AAG03434 exoenzyme T [<i>Pseudomonas aeruginosa</i>]
	17	NP_047619 Yop targeted effector [<i>Yersinia pestis</i>] YopT
25	18	NP_052380 protein kinase YopO [<i>Yersinia enterocolitica</i>]
	19	AAF82095 outer protein AvrA [<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Dublin]
30	20	AAC44300 SpiC [<i>Salmonella typhimurium</i>]
	21	SigD with the first 29 codons removed, thrombin linker, diphtheria translocation domain, TeNT-H _c
35	22	SigD with the first 29 codons removed, factor Xa linker, diphtheria translocation domain, TeNT-H _c
	23	SigD with the first 29 codons removed, thrombin linker,

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diphtheria toxin translocation domain, with BoNT/F-H_C

5	24	SigD, factor Xa linker, diphtheria toxin translocation domain, with BoNT/F-H _C
	25	YopT, factor Xa linker, diphtheria translocation domain, TeNT-H _C
10	26	YopT, factor Xa linker, diphtheria toxin translocation domain, with BoNT/F-H _C
	27	SpiC, thrombin linker, diphtheria translocation domain, TeNT-H _C
15	28	SpiC, factor Xa linker, diphtheria translocation domain, TeNT-H _C
20	29	SpiC fused to a domain consisting the N-terminal 254 residues from <i>Bacillus anthracis</i> lethal factor capable of interacting with protective antigen
	30	<i>Bacillus anthracis</i> protective antigen
25	31	<i>Clostridium botulinum</i> C2 toxin component 1
	32	<i>Clostridium botulinum</i> C2 toxin component 2

- 40 -

Table 1: Examples of type III and type IV effectors and their activity.

	Effector	Biochemical function	Possible applications
5	YopT <i>Yersinia spp</i>	Inactivates Rho GTPases by direct	Stimulate nerve regrowth following damage
	ExoS (N-terminal domain) <i>Pseudomonas aeruginosa</i>	GTPase activating protein for Rho GTPases	Stimulate nerve regrowth
10	YopE <i>Yersinia spp</i>		
	ExoS (C-terminal domain) <i>P.aeruginosa</i>	ADP-ribosyltransferase modifies Ras and Rap GTPases	Block Ras/Rap signalling pathways
	SptP (N-terminal domain) <i>Salmonella spp</i>	GAP activity for Rac 1/ Cdc 42	
15	SopE/E2 <i>S.typhimurium</i>	Guanine nucleotide exchange factor for Cdc42/Rac	Regulates nitric oxide release
	YpkO/YopO <i>Yersinia spp</i>	Serine/threonine kinase modifies RhoA/Rac	
	YopP/YopJ <i>Yersinia spp</i>	Blocks activation of various MAP kinase pathways	Induction of apoptosis in tumour cells
20	AvrXv/AvrBsT <i>Xanthomonas campestris</i>		Block release of inflammatory mediators from damaged cells
	SopB/SigA/SigD <i>Salmonella spp</i>	Activate AKT kinase	Block apoptosis in damaged/ageing neurons
25	IpgD <i>Shigella flexneri</i>	Block endosome fusion	Prevent neurotransmitter release from pain fibres
	SpiC <i>S.enterica</i>		Induction of apoptosis in glioma/neuroblastoma cells
	IpaB	Induces apoptosis by direct activation of caspase 1	Modulation of induction of cell death and other mitochondrial functions
	SipB		
	Orf19 <i>E.coli</i>	Affects mitochondrial function	
30	IpgB <i>Shigella flexneri</i>		
	Unidentified effector <i>Chlamydia spp</i>	Blocks apoptosis	Prevent apoptosis in damaged/ageing neurones
	RalF <i>Listeria monocytogenes</i>	Guanine nucleotide exchange factor for ARF	Promote or prevent membrane compartment fusion
35	SpiC, SopE, SseE,F,G or J, PipA or B, SifA or B, <i>Salmonella spp.</i> RalF, <i>Listeria monocytogenes</i> CagA <i>Helicobacter pylori</i>	Various	Treating intracellular pathogens or disorders of intracellular trafficking
		Cytoskeletal modification	Alter uptake or release of membrane vesicle contents
40	YopM <i>Yersinia spp</i> , PopC <i>Ralstonia solanacearum</i>	Leucine rich repeat protein. Possible transcription factors	Upregulation of genes involved in cell cycle and cell growth (YopM) or other genes.

CLAIMS

1. A conjugate of an injected bacterial effector protein and a carrier that targets the effector protein to a target cell.
2. A conjugate according to claim 1, comprising the effector protein linked by a linker to the carrier.
3. A conjugate according to claim 2, wherein the linker is cleavable, in that it can be cleaved after entry into the target cell so as to release the effector from the carrier.
4. A conjugate according to any previous claim, wherein the carrier targets the effector to a cell selected from an epithelial cell, a neuronal cell, a secretory cell, an immunological cell, an endocrine cell, an inflammatory cell, an exocrine cell, a bone cell and a cell of the cardiovascular system.
5. A conjugate according to any previous claim, wherein the carrier is a cell targeting component that comprises a first domain targeting the effector to a target cell and a second domain that translocates the effector into the cytosol of the cell.
6. A conjugate according to any previous claim, which is a single polypeptide.
7. A conjugate according to any previous claim, wherein the injected bacterial effector protein has an activity selected from activating GTPase, inactivating GTPase, enhancing replacement of bound GDP by GTP, causing covalent modification of GTPase, protein kinase activity, protein phosphatase, inositol phosphatase activity, inhibition of mitogen activated protein kinase kinase, regulation of gene expression, transcription factor and modulation of cellular trafficking.
8. A pharmaceutical composition comprising a conjugate according to any previous claim.

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- 5
9. A pharmaceutical composition comprising a conjugate according to claims 1-7 for a treatment selected from promoting survival of cells, preventing damage to cells, reversing damage to cells, promoting growth of cells, inhibiting apoptosis, inhibiting release of an inflammatory mediator from cells, promoting division of cells and treating intracellular infection.
- 10
10. A pharmaceutical composition according to claims 8 or 9, for treating intracellular infection.
- 15
11. A pharmaceutical composition according to any of claims 8-10, for a treatment selected from inhibiting survival of cells, inhibiting growth of cells, inhibiting division of cells, promoting apoptosis, killing cells, promoting release of an inflammatory mediator from cells, regulating nitric oxide release from cells, inhibiting secretion from cells, interfering with intracellular trafficking and modulating expression of cell-surface markers.
- 20
12. A pharmaceutical composition according to claim 11, for interfering with intracellular trafficking.
- 25
13. A pharmaceutical composition according to claim 11, for modulating expression of cell-surface markers.
- 30
14. A pharmaceutical composition according to claim 11, for inhibiting secretion from cells
- 35
15. A pharmaceutical composition according to any of claims 8-14, for treatment of neuronal cells.
16. A pharmaceutical composition according to Claim 15, for promoting survival of neuronal cells.
17. A DNA construct encoding a conjugate according to any of claims 1-7.
18. A pharmaceutical composition, comprising the DNA construct of claim

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17.

19. A pharmaceutical composition, comprising a vector containing the DNA construct of claim 17.

20. A pharmaceutical composition for delivery of an injected bacterial effector protein to a cell, comprising:-
the effector protein; linked by a cleavable linker to
a cell targeting component, comprising a first domain that binds to a cell and a second domain that translocates the effector protein of the composition into the cell.

21. A composition according to Claim 20 wherein the first domain is selected from (a) neuronal cell binding domains of clostridial toxins; and (b) fragments, variants and derivatives of the domains in (a) that substantially retain the neuronal cell binding activity of the domains of (a).

22. A composition according to Claim 20 or 21 wherein the second domain is selected from (a) domains of clostridial neurotoxins that translocate polypeptide sequences into cells, and (b) fragments, variants and derivatives of the domains of (a) that substantially retain the translocating activity of the domains of (a).

23. A composition according to Claim 20 or 21 wherein the second domain is selected from:-
(a) a translocation domain that is not a H_N domain of a clostridial toxin and is not a fragment or derivative of a H_N domain of a clostridial toxin;
(b) a non-aggregating translocation domain as measured by size in physiological buffers;
(c) a H_N domain of a diphtheria toxin,
(d) a fragment or derivative of (c) that substantially retains the translocating activity of the H_N domain of a diphtheria toxin,
(e) a fusogenic peptide,
(f) a membrane disrupting peptide, and
(g) translocating fragments and derivatives of (e) and (f).

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24. A composition according to any of Claims 20 to 23 wherein the linker is cleaved in the neuronal cell so as to release the effector protein from the targeting component.
- 5 25. A composition according to Claim 24, wherein the linker is a disulphide bridge or a site for a protease found in the target cell.
26. A method of preparation of a conjugate according to any of claims 1 to 7 by combining the effector protein with the carrier.
- 10 27. A method according to claim 26, comprising chemically linking the effector protein with the carrier.
- 15 28. A method according to claim 26, comprising expressing a DNA that encodes a polypeptide having a first region that corresponds to the effector protein and a second region that codes for the carrier.
- 20 29. A method according to any of claims 26 to 28, wherein the polypeptide includes a third region, between the first and second regions, which is cleaved by a proteolytic enzyme present in the target cell.
- 25 30. A method according to any of claims 26 to 29, comprising linking the polypeptide between the first and second region and linking the first and second regions via a disulphide bridge.
- 30 31. Use of a conjugate of an injected bacterial effector protein and a carrier that targets the effector protein to a target cell in manufacture of a medicament.
32. Use of a DNA construct encoding a conjugate of an injected bacterial effector protein and a carrier that targets the effector protein to a target cell in manufacture of a medicament.
- 35 33. Use according to claims 31 or 32 in manufacture of a medicament for treatment of a neuronal cell.

- 45 -

34. Use according to claims 31 or 32 in manufacture of a medicament for treating intracellular infection.
- 5 35. Use according to claims 31 or 32 in manufacture of a medicament for interfering with intracellular trafficking.
36. Use according to claims 31 or 32 in manufacture of a medicament for modulating expression of cell-surface markers.
- 10 37. Use according to claims 31 or 32 in manufacture of a medicament for inhibiting secretion from cells.
38. Use of an injected bacterial effector protein in manufacture of a medicament for treatment of a neuronal cell.
- 15 39. Use of an injected bacterial effector protein in manufacture of a medicament for treating intracellular infection.
40. Use of an injected bacterial effector protein in manufacture of a medicament for interfering with intracellular trafficking.
- 20 41. Use of an injected bacterial type effector protein in manufacture of a medicament for modulating expression of cell-surface markers.
42. Use of an injected bacterial effector protein in manufacture of a medicament for inhibiting secretion from cells.
- 25 43. Use of a DNA construct encoding an injected bacterial effector protein in manufacture of a medicament for treatment of a neuronal cell.
- 30 44. Use of a DNA construct encoding an injected bacterial effector protein in manufacture of a medicament for treating intracellular infection.
- 35 45. Use of a DNA construct encoding an injected bacterial effector protein in manufacture of a medicament for interfering with

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intracellular trafficking.

- 5 46. Use of a DNA construct encoding an injected bacterial effector protein in manufacture of a medicament for modulating expression of cell-surface markers.
- 10 47. Use of a DNA construct encoding an injected bacterial effector protein in manufacture of a medicament for inhibiting secretion from cells.
48. A method of delivering an injected bacterial effector protein to a neuronal cell comprising administering a composition according to any of Claims 19 to 24.
- 15 49. A method according to Claim 46 comprising injecting the composition.

-1-

SEQUENCE LISTING

<110> Microbiological Research Authority

Clifford, Shone C

John, Sutton M

Nigel, Silman

<120> Pharmaceutical use of secreted bacterial effector proteins

<130> GWS/PG/23433

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<170> PatentIn version 3.1

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20 25 30

Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu
35 40 45

Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu His
50 55 60

Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val Phe
65 70 75 80

Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val Ile
85 90 95

-2-

Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser
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Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val
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His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser
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Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile
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Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe Gln
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Arg Ser
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 20 25 30

Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser
 35 40 45

Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu
 50 55 60

Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro
 65 70 75 80

Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln

-3-

	85		90		95
Val Ile Asp	Ser Glu Thr Ala Asp	Asn Leu Glu Lys Thr	Thr Ala Ala		
	100	105	110		
Leu Ser Ile	Leu Pro Gly Ile Gly	Ser Val Met Gly	Ile Ala Asp Gly		
	115	120	125		
Ala Val His	His Asn Thr Glu Glu	Ile Val Ala Gln	Ser Ile Ala Leu		
	130	135	140		
Ser Ser Leu	Met Val Ala Gln Ala	Ile Pro Leu Val	Gly Glu Leu Val		
	145	150	155	160	
Asp Ile Gly	Phe Ala Ala Tyr Asn	Phe Val Glu Ser	Ile Ile Asn Leu		
	165	170	175		
Phe Gln Val	Val His Asn Ser Tyr	Asn Arg Pro Ala	Tyr Ser Pro Gly		
	180	185	190		
His Lys Thr	Gln Pro Phe Leu His	Asp Gly Tyr Ala	Val Ser Trp Asn		
	195	200	205		
Thr Val Arg	Ser Lys Asn Leu Asp	Cys Trp Val Asp	Asn Glu Glu Asp		
	210	215	220		
Ile Asp Val	Ile Leu Lys Lys Ser	Thr Ile Leu Asn	Leu Asp Ile Asn		
	225	230	235	240	
Asn Asp Ile	Ile Ser Asp Ile Ser	Gly Phe Asn Ser	Ser Val Ile Thr		
	245	250	255		
Tyr Pro Asp	Ala Gln Leu Val Pro	Gly Ile Asn Gly	Lys Ala Ile His		
	260	265	270		
Leu Val Asn	Asn Glu Ser Ser Glu	Val Ile Val His	Lys Ala Met Asp		
	275	280	285		
Ile Glu Tyr	Asn Asp Met Phe	Asn Asn Phe Thr	Val Ser Phe Trp	Leu	
	290	295	300		
Arg Val Pro	Lys Val Ser Ala Ser	His Leu Glu Gln	Tyr Gly Thr Asn		
	305	310	315	320	
Glu Tyr Ser	Ile Ile Ser Ser Met	Lys Lys His Ser	Leu Ser Ile Gly		
	325	330	335		
Ser Gly Trp	Ser Val Ser Leu Lys	Gly Asn Asn Leu	Ile Trp Thr Leu		
	340	345	350		

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Lys Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro
 355 360 365

Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile
 370 375 380

Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu
 385 390 395 400

Met Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn
 405 410 415

Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val
 420 425 430

Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu
 435 440 445

Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp
 450 455 460

Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro
 465 470 475 480

Val Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr
 485 490 495

Met Tyr Leu Thr Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile
 500 505 510

Tyr Tyr Arg Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr
 515 520 525

Thr Pro Asn Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile
 530 535 540

Lys Leu Tyr Val Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro
 545 550 555 560

Lys Asp Gly Asn Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly
 565 570 575

Tyr Asn Ala Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys
 580 585 590

Leu Arg Asp Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp
 595 600 605

Lys Asn Ala Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly
 610 615 620

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Asn Asp Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn
625 630 635 640

His Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr
645 650 655

Asp Glu Gly Trp Thr Asn Asp Leu Gln
660 665

<210> 3

<211> 677

<212> PRT

<213> thrombin linker, diphtheria toxin translocation domain, TeNT-HC

<400> 3

Arg Ser Cys Gly Leu Val Pro Arg Gly Ser Gly Pro Gly Ser Ser Val
1 5 10 15

Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg Asp
20 25 30

Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly Pro Ile Lys
35 40 45

Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu Lys Ala
50 55 60

Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu His Pro Glu
65 70 75 80

Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val Phe Ala Gly
85 90 95

Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser
100 105 110

Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu
115 120 125

Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His His
130 135 140

Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser Leu Met
145 150 155 160

Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile Gly Phe

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165								170				175			
Ala	Ala	Tyr	Asn 180	Phe	Val	Glu	Ser	Ile 185	Ile	Asn	Leu	Phe	Gln 190	Val	Val
His	Asn 195	Ser	Tyr	Asn	Arg	Pro	Ala 200	Tyr	Ser	Pro	Gly	His 205	Lys	Thr	Gln
Pro	Phe 210	Leu	His	Asp	Gly	Tyr 215	Ala	Val	Ser	Trp	Asn 220	Thr	Val	Arg	Ser
Lys 225	Asn	Leu	Asp	Cys	Trp 230	Val	Asp	Asn	Glu	Glu 235	Asp	Ile	Asp	Val	Ile 240
Leu	Lys	Lys	Ser	Thr 245	Ile	Leu	Asn	Leu	Asp 250	Ile	Asn	Asn	Asp	Ile 255	Ile
Ser	Asp	Ile	Ser 260	Gly	Phe	Asn	Ser	Ser 265	Val	Ile	Thr	Tyr	Pro 270	Asp	Ala
Gln	Leu	Val 275	Pro	Gly	Ile	Asn	Gly 280	Lys	Ala	Ile	His	Leu 285	Val	Asn	Asn
Glu	Ser 290	Ser	Glu	Val	Ile	Val 295	His	Lys	Ala	Met	Asp 300	Ile	Glu	Tyr	Asn
Asp 305	Met	Phe	Asn	Asn	Phe 310	Thr	Val	Ser	Phe	Trp 315	Leu	Arg	Val	Pro	Lys 320
Val	Ser	Ala	Ser	His 325	Leu	Glu	Gln	Tyr	Gly 330	Thr	Asn	Glu	Tyr	Ser 335	Ile
Ile	Ser	Ser	Met 340	Lys	Lys	His	Ser	Leu 345	Ser	Ile	Gly	Ser	Gly 350	Trp	Ser
Val	Ser	Leu 355	Lys	Gly	Asn	Asn	Leu 360	Ile	Trp	Thr	Leu	Lys 365	Asp	Ser	Ala
Gly	Glu 370	Val	Arg	Gln	Ile	Thr 375	Phe	Arg	Asp	Leu	Pro 380	Asp	Lys	Phe	Asn
Ala 385	Tyr	Leu	Ala	Asn	Lys 390	Trp	Val	Phe	Ile	Thr 395	Ile	Thr	Asn	Asp	Arg 400
Leu	Ser	Ser	Ala	Asn 405	Leu	Tyr	Ile	Asn	Gly 410	Val	Leu	Met	Gly	Ser 415	Ala
Glu	Ile	Thr	Gly 420	Leu	Gly	Ala	Ile	Arg 425	Glu	Asp	Asn	Asn	Ile 430	Thr	Leu

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Lys Leu Asp Arg Cys Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys
 435 440 445

Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu
 450 455 460

Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn
 465 470 475 480

Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser
 485 490 495

Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr
 500 505 510

Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg
 515 520 525

Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn
 530 535 540

Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val
 545 550 555 560

Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn
 565 570 575

Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro
 580 585 590

Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu
 595 600 605

Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser
 610 615 620

Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro Asn
 625 630 635 640

Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His Leu Lys Asp
 645 650 655

Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp Glu Gly Trp
 660 665 670

Thr Asn Asp Leu Gln
 675

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<211> 677

<212> PRT

<213> factor Xa linker, Diphtheria toxin translocation domain, TeNT-HC

<400> 4

Arg Ser Cys Gly Ile Glu Gly Arg Ala Pro Gly Pro Gly Ser Ser Val
 1 5 10 15

Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg Asp
 20 25 30

Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly Pro Ile Lys
 35 40 45

Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu Lys Ala
 50 55 60

Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu His Pro Glu
 65 70 75 80

Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val Phe Ala Gly
 85 90 95

Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser
 100 105 110

Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu
 115 120 125

Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His His
 130 135 140

Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser Leu Met
 145 150 155 160

Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile Gly Phe
 165 170 175

Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe Gln Val Val
 180 185 190

His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His Lys Thr Gln
 195 200 205

Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr Val Arg Ser
 210 215 220

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Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp Val Ile
 225 230 235 240

Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile
 245 250 255

Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala
 260 265 270

Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn
 275 280 285

Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn
 290 295 300

Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys
 305 310 315 320

Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile
 325 330 335

Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly Trp Ser
 340 345 350

Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala
 355 360 365

Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn
 370 375 380

Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn Asp Arg
 385 390 395 400

Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly Ser Ala
 405 410 415

Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu
 420 425 430

Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys
 435 440 445

Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu
 450 455 460

Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn
 465 470 475 480

Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser
 485 490 495

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Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr
 500 505 510

Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg
 515 520 525

Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn
 530 535 540

Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val
 545 550 555 560

Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn
 565 570 575

Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro
 580 585 590

Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu
 595 600 605

Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser
 610 615 620

Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro Asn
 625 630 635 640

Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His Leu Lys Asp
 645 650 655

Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp Glu Gly Trp
 660 665 670

Thr Asn Asp Leu Gln
 675

<210> 5

<211> 645

<212> PRT

<213> diphtheria toxin translocation domain with BoNT/F-HC

<400> 5

Gly Ser Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp
 1 5 10 15

Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His

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20	25	30
Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser		
35	40	45
Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu		
50	55	60
Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro		
65	70	75
Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln		
85	90	95
Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala		
100	105	110
Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly		
115	120	125
Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu		
130	135	140
Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val		
145	150	155
Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu		
165	170	175
Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly		
180	185	190
His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn		
195	200	205
Thr Val Arg Ser Thr Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu		
210	215	220
Tyr Phe Asn Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp		
225	230	235
Met Arg Tyr Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser		
245	250	255
Asn Ile Ser Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn		
260	265	270
Gln Phe Gly Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln		
275	280	285

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Asn Asn Asp Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser
 290 295 300

Phe Trp Val Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn
 305 310 315 320

Glu Tyr Thr Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys
 325 330 335

Ile Ser Leu Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala
 340 345 350

Gly Asn Asn Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile
 355 360 365

Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg
 370 375 380

Leu Gly Asn Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys
 385 390 395 400

Ser Ile Ser Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe
 405 410 415

Lys Ile Val Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe
 420 425 430

Lys Val Phe Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr
 435 440 445

Ser Asp Glu Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr
 450 455 460

Leu Leu Tyr Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp
 465 470 475 480

Lys Ser Ile Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg
 485 490 495

Gly Val Tyr Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr
 500 505 510

Gly Val Glu Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn
 515 520 525

Thr Asp Asn Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val
 530 535 540

Asp Arg Asp Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys
 545 550 555 560

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Pro Glu Lys Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser
565 570 575

Leu Gly Gln Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met
580 585 590

Asn Phe Gln Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His
595 600 605

Ser Asn Asn Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys
610 615 620

Asn Thr Ser Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His
625 630 635 640

Gly Trp Gln Glu Asn
645

<210> 6

<211> 657

<212> PRT

<213> thrombin linker, diphtheria toxin translocation domain, BoNT/F-HC

<400> 6

Arg Ser Cys Gly Leu Val Pro Arg Gly Ser Gly Pro Gly Ser Ser Val
1 5 10 15

Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg Asp
20 25 30

Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly Pro Ile Lys
35 40 45

Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu Lys Ala
50 55 60

Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu His Pro Glu
65 70 75 80

Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val Phe Ala Gly
85 90 95

Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser
100 105 110

Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu

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115	120	125
Pro Gly Ile Gly Ser Val Met 130 135	Gly Ile Ala Asp Gly Ala Val His His 140	
Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser Leu Met 145 150 155 160		
Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile Gly Phe 165 170 175		
Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe Gln Val Val 180 185 190		
His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His Lys Thr Gln 195 200 205		
Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr Val Arg Ser 210 215 220		
Thr Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys 225 230 235 240		
Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu 245 250 255		
Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile 260 265 270		
Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile 275 280 285		
Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile 290 295 300		
Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg 305 310 315 320		
Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile 325 330 335		
Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn 340 345 350		
Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln 355 360 365		
Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile 370 375 380		

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Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser
385 390 395 400

Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn
405 410 415

Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly
420 425 430

Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp
435 440 445

Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro
450 455 460

Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn
465 470 475 480

Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr
485 490 495

Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln
500 505 510

Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val
515 520 525

Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe
530 535 540

Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val
545 550 555 560

Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile
565 570 575

Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile
580 585 590

Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn
595 600 605

Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu
610 615 620

Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser
625 630 635 640

Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu
645 650 655

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Asn

<210> 7

<211> 657

<212> PRT

<213> factor Xa linker, diphtheria toxin translocation domain,
BoNT/F-Hc

<400> 7

Arg Ser Cys Gly Ile Glu Gly Arg Ala Pro Gly Pro Gly Ser Ser Val
1 5 10 15

Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg Asp
20 25 30

Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly Pro Ile Lys
35 40 45

Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu Lys Ala
50 55 60

Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu His Pro Glu
65 70 75 80

Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val Phe Ala Gly
85 90 95

Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser
100 105 110

Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu
115 120 125

Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His His
130 135 140

Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser Leu Met
145 150 155 160

Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile Gly Phe
165 170 175

Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe Gln Val Val
180 185 190

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His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His Lys Thr Gln
 195 200 205

Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr Val Arg Ser
 210 215 220

Thr Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys
 225 230 235 240

Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu
 245 250 255

Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile
 260 265 270

Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile
 275 280 285

Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile
 290 295 300

Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg
 305 310 315 320

Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile
 325 330 335

Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn
 340 345 350

Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln
 355 360 365

Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile
 370 375 380

Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser
 385 390 395 400

Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn
 405 410 415

Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly
 420 425 430

Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp
 435 440 445

Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro
 450 455 460

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Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn
 465 470 475 480

Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr
 485 490 495

Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln
 500 505 510

Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val
 515 520 525

Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe
 530 535 540

Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val
 545 550 555 560

Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile
 565 570 575

Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile
 580 585 590

Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn
 595 600 605

Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu
 610 615 620

Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser
 625 630 635 640

Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu
 645 650 655

Asn

<210> 8

<211> 563

<212> PRT

<213> AAC46234 invasion gene D protein [Salmonella typhimurium] SigD

<400> 8

Met Gln Ile Gln Ser Phe Tyr His Ser Ala Ser Leu Lys Thr Gln Glu

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1	5	10	15
Ala Phe Lys Ser Leu Gln Lys Thr Leu Tyr Asn Gly Met Gln Ile Leu	20	25	30
Ser Gly Gln Gly Lys Ala Pro Ala Lys Ala Pro Asp Ala Arg Pro Glu	35	40	45
Ile Ile Val Leu Arg Glu Pro Gly Ala Thr Trp Gly Asn Tyr Leu Gln	50	55	60
His Gln Lys Ala Ser Asn His Ser Leu His Asn Leu Tyr Asn Leu Gln	65	70	75
Arg Asp Leu Leu Thr Val Ala Ala Thr Val Leu Gly Lys Gln Asp Pro	85	90	95
Val Leu Thr Ser Met Ala Asn Gln Met Glu Leu Ala Lys Val Lys Ala	100	105	110
Asp Arg Pro Ala Thr Lys Gln Glu Glu Ala Ala Ala Lys Ala Leu Lys	115	120	125
Lys Asn Leu Ile Glu Leu Ile Ala Ala Arg Thr Gln Gln Gln Asp Gly	130	135	140
Leu Pro Ala Lys Glu Ala His Arg Phe Ala Ala Val Ala Phe Arg Asp	145	150	155
Ala Gln Val Lys Gln Leu Asn Asn Gln Pro Trp Gln Thr Ile Lys Asn	165	170	175
Thr Leu Thr His Asn Gly His His Tyr Thr Asn Thr Gln Leu Pro Ala	180	185	190
Ala Glu Met Lys Ile Gly Ala Lys Asp Ile Phe Pro Ser Ala Tyr Glu	195	200	205
Gly Lys Gly Val Cys Ser Trp Asp Thr Lys Asn Ile His His Ala Asn	210	215	220
Asn Leu Trp Met Ser Thr Val Ser Val His Glu Asp Gly Lys Asp Lys	225	230	235
Thr Leu Phe Phe Asp Gly Ile Arg His Gly Val Leu Ser Pro Tyr His	245	250	255
Glu Lys Asp Pro Leu Leu Arg His Val Gly Ala Glu Asn Lys Ala Lys	260	265	270

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Glu Val Leu Thr Ala Ala Leu Phe Ser Lys Pro Glu Leu Leu Asn Lys
 275 280 285

Ala Leu Ala Gly Glu Ala Val Ser Leu Lys Leu Val Ser Val Gly Leu
 290 295 300

Leu Thr Ala Ser Asn Ile Phe Gly Lys Glu Gly Thr Met Val Glu Asp
 305 310 315 320

Gln Met Arg Ala Trp Gln Ser Leu Thr Gln Pro Gly Lys Met Ile His
 325 330 335

Leu Lys Ile Arg Asn Lys Asp Gly Asp Leu Gln Thr Val Lys Ile Lys
 340 345 350

Pro Asp Val Val Ala Ala Phe Asn Val Gly Val Asn Glu Leu Ala Leu
 355 360 365

Lys Leu Gly Phe Gly Leu Lys Ala Ser Asp Ser Tyr Asn Ala Glu Ala
 370 375 380

Leu His Gln Leu Leu Gly Asn Asp Leu Arg Pro Glu Ala Arg Pro Gly
 385 390 395 400

Gly Trp Val Gly Glu Trp Leu Ala Gln Tyr Pro Asp Asn Tyr Glu Val
 405 410 415

Val Asn Thr Leu Ala Arg Gln Ile Lys Asp Ile Trp Lys Asn Asn Gln
 420 425 430

His His Lys Asp Gly Gly Glu Pro Tyr Lys Leu Ala Gln Arg Leu Ala
 435 440 445

Met Leu Ala His Glu Ile Asp Ala Val Pro Ala Trp Asn Cys Lys Ser
 450 455 460

Gly Lys Asp Arg Thr Gly Met Met Asp Ser Glu Ile Lys Gly Glu Ile
 465 470 475 480

Ile Ser Leu His Gln Thr His Met Leu Ser Ala Pro Gly Ser Leu Pro
 485 490 495

Asp Ser Gly Gly Gln Lys Ile Phe Gln Lys Val Leu Leu Asn Ser Gly
 500 505 510

Asn Leu Glu Ile Gln Lys Gln Asn Thr Gly Gly Ala Gly Asn Lys Val
 515 520 525

Met Lys Asn Leu Ser Pro Glu Val Leu Asn Leu Ser Tyr Gln Lys Arg
 530 535 540

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Val Gly Asp Glu Asn Ile Trp Gln Ser Val Lys Gly Ile Ser Ser Leu
 545 550 555 560

Ile Thr Ser

<210> 9

<211> 433

<212> PRT

<213> AAF21057 invasion protein D [Salmonella typhimurium] SopB

<400> 9

Val Leu Thr Ser Met Ala Asn Gln Met Glu Leu Ala Lys Val Lys Ala
 1 5 10 15

Asp Arg Pro Ala Thr Lys Gln Glu Glu Ala Ala Ala Lys Ala Leu Lys
 20 25 30

Lys Asn Leu Ile Glu Leu Ile Ala Ala Arg Thr Gln Gln Gln Asp Gly
 35 40 45

Leu Pro Ala Lys Glu Ala His Arg Phe Ala Ala Val Ala Phe Arg Asp
 50 55 60

Ala Gln Val Lys Gln Leu Asn Asn Gln Pro Trp Gln Thr Ile Lys Asn
 65 70 75 80

Thr Leu Thr His Asn Gly His His Tyr Thr Asn Thr Gln Leu Pro Ala
 85 90 95

Ala Glu Met Lys Ile Gly Ala Lys Asp Ile Phe Pro Ser Ala Tyr Glu
 100 105 110

Gly Lys Gly Val Cys Ser Trp Asp Thr Lys Asn Ile His His Ala Asn
 115 120 125

Asn Leu Trp Met Ser Thr Val Ser Val His Glu Asp Gly Lys Asp Lys
 130 135 140

Thr Leu Phe Cys Gly Ile Arg His Gly Val Leu Ser Pro Tyr His Glu
 145 150 155 160

Lys Asp Pro Leu Leu Arg His Val Gly Ala Glu Asn Lys Ala Lys Glu
 165 170 175

Val Leu Thr Ala Ala Leu Phe Ser Lys Pro Glu Leu Leu Asn Lys Ala

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180							185							190						
Leu	Ala	Gly	Glu	Ala	Val	Ser	Leu	Lys	Leu	Val	Ser	Val	Gly	Leu	Leu					
		195					200					205								
Thr	Ala	Ser	Asn	Ile	Phe	Gly	Lys	Glu	Gly	Thr	Met	Val	Glu	Asp	Gln					
	210					215					220									
Met	Arg	Ala	Trp	Gln	Ser	Leu	Thr	Gln	Pro	Gly	Lys	Met	Ile	His	Leu					
225					230					235					240					
Lys	Ile	Arg	Asn	Lys	Asp	Gly	Asp	Leu	Gln	Thr	Val	Lys	Ile	Lys	Pro					
				245					250					255						
Asp	Val	Ala	Ala	Phe	Asn	Val	Gly	Val	Asn	Glu	Leu	Ala	Leu	Lys	Leu					
			260					265					270							
Gly	Phe	Gly	Leu	Lys	Ala	Ser	Asp	Ser	Tyr	Asn	Ala	Glu	Ala	Leu	His					
		275						280					285							
Gln	Leu	Leu	Gly	Asn	Asp	Leu	Arg	Pro	Glu	Ala	Arg	Pro	Gly	Gly	Trp					
	290					295					300									
Val	Gly	Glu	Trp	Leu	Ala	Gln	Tyr	Pro	Asp	Asn	Tyr	Glu	Val	Val	Asn					
305					310					315					320					
Thr	Leu	Ala	Arg	Gln	Ile	Lys	Asp	Ile	Trp	Lys	Asn	Asn	Gln	His	His					
				325					330					335						
Lys	Asp	Gly	Gly	Glu	Pro	Tyr	Lys	Leu	Ala	Gln	Arg	Leu	Ala	Met	Leu					
			340					345					350							
Ala	His	Glu	Ile	Asp	Ala	Val	Pro	Ala	Trp	Asn	Cys	Lys	Ser	Gly	Lys					
		355						360					365							
Asp	Arg	Thr	Gly	Met	Met	Asp	Ser	Glu	Ile	Lys	Arg	Glu	Ile	Ile	Ser					
	370					375					380									
Leu	His	Gln	Thr	His	Met	Leu	Ser	Ala	Pro	Gly	Ser	Leu	Pro	Asp	Ser					
385					390					395					400					
Gly	Gly	Gln	Lys	Ile	Phe	Gln	Lys	Val	Leu	Leu	Asn	Ser	Gly	Asn	Leu					
				405					410					415						
Glu	Ile	Gln	Lys	Gln	Asn	Thr	Gly	Gly	Ala	Gly	Asn	Lys	Val	Met	Lys					
				420				425					430							

Asn

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<210> 10

<211> 538

<212> PRT

<213> CAC05808 IpgD, secreted by the Mxi-Spa machinery, modulates entry of bacteria into epithelial cells [Shigella flexneri]

<400> 10

Met His Ile Thr Asn Leu Gly Leu His Gln Val Ser Phe Gln Ser Gly
1 5 10 15

Asp Ser Tyr Lys Gly Ala Glu Glu Thr Gly Lys His Lys Gly Val Ser
20 25 30

Val Ile Ser Tyr Gln Arg Val Lys Asn Gly Glu Arg Asn Lys Gly Ile
35 40 45

Glu Ala Leu Asn Arg Leu Tyr Leu Gln Asn Gln Thr Ser Leu Thr Gly
50 55 60

Lys Ser Leu Leu Phe Ala Arg Asp Lys Ala Glu Val Phe Cys Glu Ala
65 70 75 80

Ile Lys Leu Ala Gly Gly Asp Thr Ser Lys Ile Lys Ala Met Met Glu
85 90 95

Arg Leu Asp Thr Tyr Lys Leu Gly Glu Val Asn Lys Arg His Ile Asn
100 105 110

Glu Leu Asn Lys Val Ile Ser Glu Glu Ile Arg Ala Gln Leu Gly Ile
115 120 125

Lys Asn Lys Lys Glu Leu Gln Thr Lys Ile Lys Gln Ile Phe Thr Asp
130 135 140

Tyr Leu Asn Asn Lys Asn Trp Gly Pro Val Asn Lys Asn Ile Ser His
145 150 155 160

His Gly Lys Asn Tyr Ser Phe Gln Leu Thr Pro Ala Ser His Met Lys
165 170 175

Ile Gly Asn Lys Asn Ile Phe Val Lys Glu Tyr Asn Gly Lys Gly Ile
180 185 190

Cys Cys Ala Ser Thr Arg Glu Arg Asp His Ile Ala Asn Met Trp Leu
195 200 205

Ser Lys Val Val Asp Asp Glu Gly Lys Glu Ile Phe Ser Gly Ile Arg

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210	215	220
His Gly Val Ile Ser Ala Tyr Gly Leu Lys Lys Asn Ser Ser Glu Arg 225 230 235 240		
Ala Val Ala Ala Arg Asn Lys Ala Glu Glu Leu Val Ser Ala Ala Leu 245 250 255		
Tyr Ser Arg Pro Glu Leu Leu Ser Gln Ala Leu Ser Gly Lys Thr Val 260 265 270		
Asp Leu Lys Ile Val Ser Thr Ser Leu Leu Thr Pro Thr Ser Leu Thr 275 280 285		
Gly Gly Glu Glu Ser Met Leu Lys Asp Gln Val Ser Ala Leu Lys Gly 290 295 300		
Leu Asn Ser Lys Arg Gly Gly Pro Thr Lys Leu Leu Ile Arg Asn Ser 305 310 315 320		
Asp Gly Leu Leu Lys Glu Val Ser Val Asn Leu Lys Val Val Thr Phe 325 330 335		
Asn Phe Gly Val Asn Glu Leu Ala Leu Lys Met Gly Leu Gly Trp Arg 340 345 350		
Asn Val Asp Lys Leu Asn Asp Glu Ser Ile Cys Ser Leu Leu Gly Asp 355 360 365		
Asn Phe Leu Lys Asn Gly Val Ile Gly Gly Trp Ala Ala Glu Ala Ile 370 375 380		
Glu Lys Asn Pro Pro Cys Lys Asn Asp Val Ile Tyr Leu Ala Asn Gln 385 390 395 400		
Ile Lys Glu Ile Val Asn Asn Lys Leu Gln Lys Asn Asp Asn Gly Glu 405 410 415		
Pro Tyr Lys Leu Ser Gln Arg Val Thr Leu Leu Ala Tyr Thr Ile Gly 420 425 430		
Ala Val Pro Cys Trp Asn Cys Lys Ser Gly Lys Asp Arg Thr Gly Met 435 440 445		
Gln Asp Ala Glu Ile Lys Arg Glu Ile Ile Arg Lys His Glu Thr Gly 450 455 460		
Gln Phe Ser Gln Leu Asn Ser Lys Leu Ser Ser Glu Glu Lys Arg Leu 465 470 475 480		

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Phe Ser Thr Ile Leu Met Asn Ser Gly Asn Met Glu Ile Gln Glu Met
 485 490 495

Asn Thr Gly Val Pro Gly Asn Lys Val Met Lys Lys Leu Pro Leu Ser
 500 505 510

Ser Leu Glu Leu Ser Tyr Ser Glu Arg Ile Gly Asp Pro Lys Ile Trp
 515 520 525

Asn Met Val Lys Gly Tyr Ser Ser Phe Val
 530 535

<210> 11

<211> 288

<212> PRT

<213> AAC69766 targeted effector protein [Yersinia pestis] YopJ

<400> 11

Met Ile Gly Pro Ile Ser Gln Ile Asn Ile Ser Gly Gly Leu Ser Glu
 1 5 10 15

Lys Glu Thr Ser Ser Leu Ile Ser Asn Glu Glu Leu Lys Asn Ile Ile
 20 25 30

Thr Gln Leu Glu Thr Asp Ile Ser Asp Gly Ser Trp Phe His Lys Asn
 35 40 45

Tyr Ser Arg Met Asp Val Glu Val Met Pro Ala Leu Val Ile Gln Ala
 50 55 60

Asn Asn Lys Tyr Pro Glu Met Asn Leu Asn Leu Val Thr Ser Pro Leu
 65 70 75 80

Asp Leu Ser Ile Glu Ile Lys Asn Val Ile Glu Asn Gly Val Arg Ser
 85 90 95

Ser Arg Phe Ile Ile Asn Met Gly Glu Gly Gly Ile His Phe Ser Val
 100 105 110

Ile Asp Tyr Lys His Ile Asn Gly Lys Thr Ser Leu Ile Leu Phe Glu
 115 120 125

Pro Ala Asn Phe Asn Ser Met Gly Pro Ala Met Leu Ala Ile Arg Thr
 130 135 140

Lys Thr Ala Ile Glu Arg Tyr Gln Leu Pro Asp Cys His Phe Ser Met
 145 150 155 160

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Val Glu Met Asp Ile Gln Arg Ser Ser Ser Glu Cys Gly Ile Phe Ser
 165 170 175

Leu Ala Leu Ala Lys Lys Leu Tyr Ile Glu Arg Asp Ser Leu Leu Lys
 180 185 190

Ile His Glu Asp Asn Ile Lys Gly Ile Leu Ser Asp Gly Glu Asn Pro
 195 200 205

Leu Pro His Asp Lys Leu Asp Pro Tyr Leu Pro Val Thr Phe Tyr Lys
 210 215 220

His Thr Gln Gly Lys Lys Arg Leu Asn Glu Tyr Leu Asn Thr Asn Pro
 225 230 235 240

Gln Gly Val Gly Thr Val Val Asn Lys Lys Asn Glu Thr Ile Val Asn
 245 250 255

Arg Phe Asp Asn Asn Lys Ser Ile Val Asp Gly Lys Glu Leu Ser Val
 260 265 270

Ser Val His Lys Lys Arg Ile Ala Glu Tyr Lys Thr Leu Leu Lys Val
 275 280 285

<210> 12

<211> 180

<212> PRT

<213> AAC02071 SopE [Salmonella typhimurium]

<400> 12

Met Thr Lys Ile Thr Leu Ser Pro Gln Asn Phe Arg Ile Gln Lys Gln
 1 5 10 15

Glu Thr Thr Leu Leu Lys Glu Lys Ser Thr Glu Lys Asn Ser Leu Ala
 20 25 30

Lys Ser Ile Leu Ala Val Lys Asn His Phe Ile Glu Leu Arg Ser Lys
 35 40 45

Leu Ser Glu Arg Phe Ile Ser His Lys Asn Thr Glu Ser Ser Ala Thr
 50 55 60

His Phe His Arg Gly Ser Ala Ser Glu Gly Arg Ala Val Leu Thr Asn
 65 70 75 80

Lys Val Val Lys Asp Phe Met Leu Gln Thr Leu Asn Asp Ile Asp Ile

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	85		90		95
Arg Gly Ser	Ala Ser Lys Asp Pro	Ala Tyr Ala Ser Gln Thr Arg Glu			
	100	105		110	
Ala Ile Leu Ser	Ala Val Tyr Ser Lys Asn Lys Asp Gln Cys Cys Asn				
	115	120		125	
Leu Leu Ile Ser	Lys Gly Ile Asn Ile Ala Pro Phe Leu Gln Glu Ile				
	130	135		140	
Gly Glu Ala Ala Lys	Asn Ala Gly Leu Pro Gly Thr Thr Lys Asn Asp				
145	150	155		160	
Val Phe Thr Pro Ser	Gly Ala Gly Ala Asn Pro Phe Ile Thr Pro Leu				
	165	170		175	
Ile Ser Ser Ala					
	180				

<210> 13

<211> 543

<212> PRT

<213> AAC44349 protein tyrosine phosphatase SptP [Salmonella typhimurium]

<400> 13

Met Leu Lys Tyr	Glu Glu Arg Lys Leu Asn Asn Leu Thr Leu Ser Ser			
1	5	10		15
Phe Ser Lys Val	Gly Val Ser Asn Asp Ala Arg Leu Tyr Ile Ala Lys			
	20	25		30
Glu Asn Thr Asp	Lys Ala Tyr Val Ala Pro Glu Lys Phe Ser Ser Lys			
	35	40		45
Val Leu Thr Trp	Leu Gly Lys Met Pro Leu Phe Lys Asn Thr Glu Val			
	50	55		60
Val Gln Lys His	Thr Glu Asn Ile Arg Val Gln Asp Gln Lys Ile Leu			
65	70	75		80
Gln Thr Phe Leu	His Ala Leu Thr Glu Lys Tyr Gly Glu Thr Ala Val			
	85	90		95
Asn Asp Ala Leu	Leu Met Ser Arg Ile Asn Met Asn Lys Pro Leu Thr			
	100	105		110

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Gln Arg Leu Ala Val Gln Ile Thr Glu Cys Val Lys Ala Ala Asp Glu
 115 120 125

Gly Phe Ile Asn Leu Ile Lys Ser Lys Asp Asn Val Gly Val Arg Asn
 130 135 140

Ala Ala Leu Val Ile Lys Gly Gly Asp Thr Lys Val Ala Glu Lys Asn
 145 150 155 160

Asn Asp Val Gly Ala Glu Ser Lys Gln Pro Leu Leu Asp Ile Ala Leu
 165 170 175

Lys Gly Leu Lys Arg Thr Leu Pro Gln Leu Glu Gln Met Asp Gly Asn
 180 185 190

Ser Leu Arg Glu Asn Phe Gln Glu Met Ala Ser Gly Asn Gly Pro Leu
 195 200 205

Arg Ser Leu Met Thr Asn Leu Gln Asn Leu Asn Lys Ile Pro Glu Ala
 210 215 220

Lys Gln Leu Asn Asp Tyr Val Thr Thr Leu Thr Asn Ile Gln Val Gly
 225 230 235 240

Val Ala Arg Phe Ser Gln Trp Gly Thr Cys Gly Gly Glu Val Glu Arg
 245 250 255

Trp Val Asp Lys Ala Ser Thr His Glu Leu Thr Gln Ala Val Lys Lys
 260 265 270

Ile His Val Ile Ala Lys Glu Leu Lys Asn Val Thr Ala Glu Leu Glu
 275 280 285

Lys Ile Glu Ala Gly Ala Pro Met Pro Gln Thr Met Ser Gly Pro Thr
 290 295 300

Leu Gly Leu Ala Arg Phe Ala Val Ser Ser Ile Pro Ile Asn Gln Gln
 305 310 315 320

Thr Gln Val Lys Leu Ser Asp Gly Met Pro Val Pro Val Asn Thr Leu
 325 330 335

Thr Phe Asp Gly Lys Pro Val Ala Leu Ala Gly Ser Tyr Pro Lys Asn
 340 345 350

Thr Pro Asp Ala Leu Glu Ala His Met Lys Met Leu Leu Glu Lys Glu
 355 360 365

Cys Ser Cys Leu Val Val Leu Thr Ser Glu Asp Gln Met Gln Ala Lys

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370 375 380
 Gln Leu Pro Pro Tyr Phe Arg Gly Ser Tyr Thr Phe Gly Glu Val His
 385 390 395 400
 Thr Asn Ser Gln Lys Val Ser Ser Ala Ser Gln Gly Glu Ala Ile Asp
 405 410 415
 Gln Tyr Asn Met Gln Leu Ser Cys Gly Glu Lys Arg Tyr Thr Ile Pro
 420 425 430
 Val Leu His Val Lys Asn Trp Pro Asp His Gln Pro Leu Pro Ser Thr
 435 440 445
 Asp Gln Leu Glu Tyr Leu Ala Asp Arg Val Lys Asn Ser Asn Gln Asn
 450 455 460
 Gly Ala Pro Gly Arg Ser Ser Ser Asp Lys His Leu Pro Met Ile His
 465 470 475 480
 Cys Leu Gly Gly Val Gly Arg Thr Gly Thr Met Ala Ala Ala Leu Val
 485 490 495
 Leu Lys Asp Asn Pro His Ser Asn Leu Glu Gln Val Arg Ala Asp Phe
 500 505 510
 Arg Asp Ser Arg Asn Asn Arg Met Leu Glu Asp Ala Ser Gln Phe Val
 515 520 525
 Gln Leu Lys Ala Met Gln Ala Gln Leu Leu Met Thr Thr Ala Ser
 530 535 540

 <210> 14
 <211> 219
 <212> PRT
 <213> NP_047628 targeted effector [Yersinia pestis] YopE

 <400> 14
 Met Lys Ile Ser Ser Phe Ile Ser Thr Ser Leu Pro Leu Pro Thr Ser
 1 5 10 15
 Val Ser Gly Ser Ser Ser Val Gly Glu Met Ser Gly Arg Ser Val Ser
 20 25 30
 Gln Gln Thr Ser Asp Gln Tyr Ala Asn Asn Leu Ala Gly Arg Thr Glu
 35 40 45

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Ser Pro Gln Gly Ser Ser Leu Ala Ser Arg Ile Ile Glu Arg Leu Ser
 50 55 60

Ser Val Ala His Ser Val Ile Gly Phe Ile Gln Arg Met Phe Ser Glu
 65 70 75 80

Gly Ser His Lys Pro Val Val Thr Pro Ala Pro Thr Pro Ala Gln Met
 85 90 95

Pro Ser Pro Thr Ser Phe Ser Asp Ser Ile Lys Gln Leu Ala Ala Glu
 100 105 110

Thr Leu Pro Lys Tyr Met Gln Gln Leu Asn Ser Leu Asp Ala Glu Met
 115 120 125

Leu Gln Lys Asn His Asp Gln Phe Ala Thr Gly Ser Gly Pro Leu Arg
 130 135 140

Gly Ser Ile Thr Gln Cys Gln Gly Leu Met Gln Phe Cys Gly Gly Glu
 145 150 155 160

Leu Gln Ala Glu Ala Ser Ala Ile Leu Asn Thr Pro Val Cys Gly Ile
 165 170 175

Pro Phe Ser Gln Trp Gly Thr Ile Gly Gly Ala Ala Ser Ala Tyr Val
 180 185 190

Ala Ser Gly Val Asp Leu Thr Gln Ala Ala Asn Glu Ile Lys Gly Leu
 195 200 205

Ala Gln Gln Met Gln Lys Leu Leu Ser Leu Met
 210 215

<210> 15

<211> 453

<212> PRT

<213> AAK39624 exoenzyme S [Pseudomonas aeruginosa]

<400> 15

Met His Ile Gln Ser Leu Gln Gln Ser Pro Ser Phe Ala Val Glu Leu
 1 5 10 15

His Gln Ala Ala Ser Gly Arg Leu Gly Gln Ile Glu Ala Arg Gln Val
 20 25 30

Ala Thr Pro Ser Glu Ala Gln Gln Leu Ala Gln Arg Gln Asp Ala Pro
 35 40 45

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Lys Gly Glu Gly Leu Leu Ala Arg Leu Gly Ala Ala Leu Val Arg Pro
 50 55 60

Phe Val Ala Ile Met Asp Trp Leu Gly Lys Leu Leu Gly Ser His Ala
 65 70 75 80

Arg Thr Gly Pro Gln Pro Ser Gln Asp Ala Gln Pro Ala Val Met Ser
 85 90 95

Ser Ala Val Val Phe Lys Gln Met Val Leu Gln Gln Ala Leu Pro Met
 100 105 110

Thr Leu Lys Gly Leu Asp Lys Ala Ser Glu Leu Ala Thr Leu Thr Pro
 115 120 125

Glu Gly Leu Ala Arg Glu His Ser Arg Leu Ala Ser Gly Asp Gly Ala
 130 135 140

Leu Arg Ser Leu Ser Thr Ala Leu Ala Gly Ile Arg Ala Gly Ser Gln
 145 150 155 160

Val Glu Glu Ser Arg Ile Gln Ala Gly Arg Leu Leu Glu Arg Ser Ile
 165 170 175

Gly Gly Ile Ala Leu Gln Gln Trp Gly Thr Thr Gly Gly Ala Ala Ser
 180 185 190

Gln Leu Val Leu Asp Ala Ser Pro Glu Leu Arg Arg Glu Ile Thr Asp
 195 200 205

Gln Leu His Gln Val Met Ser Glu Val Ala Leu Leu Arg Gln Ala Val
 210 215 220

Glu Ser Glu Val Ser Arg Val Ser Ala Asp Lys Ala Leu Ala Asp Gly
 225 230 235 240

Leu Val Lys Arg Phe Gly Ala Asp Ala Glu Lys Tyr Leu Gly Arg Gln
 245 250 255

Pro Gly Gly Ile His Ser Asp Ala Glu Val Met Ala Leu Gly Leu Tyr
 260 265 270

Thr Gly Ile His Tyr Ala Asp Leu Asn Arg Ala Leu Arg Gln Gly Gln
 275 280 285

Glu Leu Asp Ala Gly Gln Lys Leu Ile Asp Gln Gly Met Ser Ala Ala
 290 295 300

Phe Glu Lys Ser Gly Gln Ala Glu Gln Val Val Lys Thr Phe Arg Gly

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305 310 315 320
 Thr Arg Gly Gly Asp Ala Phe Asn Ala Val Glu Glu Gly Lys Val Gly
 325 330 335
 His Asp Asp Gly Tyr Leu Ser Thr Ser Leu Asn Pro Gly Val Ala Arg
 340 345 350
 Ser Phe Gly Gln Gly Thr Ile Ser Thr Val Phe Gly Arg Ser Gly Ile
 355 360 365
 Asp Val Ser Gly Ile Ser Asn Tyr Lys Asn Glu Lys Glu Ile Leu Tyr
 370 375 380
 Asn Lys Glu Thr Asp Met Arg Val Leu Leu Ser Ala Ser Asp Glu Gln
 385 390 395 400
 Gly Val Thr Arg Arg Val Leu Glu Glu Ala Ala Leu Gly Glu Gln Ser
 405 410 415
 Gly His Ser Gln Gly Leu Leu Asp Ala Leu Asp Leu Ala Ser Lys Pro
 420 425 430
 Glu Arg Ser Gly Glu Val Gln Glu Gln Asp Val Arg Leu Arg Met Arg
 435 440 445
 Gly Leu Asp Leu Ala
 450

<210> 16

<211> 457

<212> PRT

<213> AAG03434 exoenzyme T [Pseudomonas aeruginosa]

<400> 16

Met His Ile Gln Ser Ser Gln Gln Asn Pro Ser Phe Val Ala Glu Leu
 1 5 10 15
 Ser Gln Ala Val Ala Gly Arg Leu Gly Gln Val Glu Ala Arg Gln Val
 20 25 30
 Ala Thr Pro Arg Glu Ala Gln Gln Leu Ala Gln Arg Gln Glu Ala Pro
 35 40 45
 Lys Gly Glu Gly Leu Leu Ser Arg Leu Gly Ala Ala Leu Ala Arg Pro
 50 55 60

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Phe Val Ala Ile Ile Glu Trp Leu Gly Lys Leu Leu Gly Ser Arg Ala
65 70 75 80

His Ala Ala Thr Gln Ala Pro Leu Ser Arg Gln Asp Ala Pro Pro Ala
85 90 95

Ala Ser Leu Ser Ala Ala Glu Ile Lys Gln Met Met Leu Gln Lys Ala
100 105 110

Leu Pro Leu Thr Leu Gly Gly Leu Gly Lys Ala Ser Glu Leu Ala Thr
115 120 125

Leu Thr Ala Glu Arg Leu Ala Lys Asp His Thr Arg Leu Ala Ser Gly
130 135 140

Asp Gly Ala Leu Arg Ser Leu Ala Thr Ala Leu Val Gly Ile Arg Asp
145 150 155 160

Gly Ser Arg Ile Glu Ala Ser Arg Thr Gln Ala Ala Arg Leu Leu Glu
165 170 175

Gln Ser Val Gly Gly Ile Ala Leu Gln Gln Trp Gly Thr Ala Gly Gly
180 185 190

Ala Ala Ser Gln His Val Leu Ser Ala Ser Pro Glu Gln Leu Arg Glu
195 200 205

Ile Ala Val Gln Leu His Ala Val Met Asp Lys Val Ala Leu Leu Arg
210 215 220

His Ala Val Glu Ser Glu Val Lys Gly Glu Pro Val Asp Lys Ala Leu
225 230 235 240

Ala Asp Gly Leu Val Glu His Phe Gly Leu Glu Ala Glu Gln Tyr Leu
245 250 255

Gly Glu His Pro Asp Gly Pro Tyr Ser Asp Ala Glu Val Met Ala Leu
260 265 270

Gly Leu Tyr Thr Asn Gly Glu Tyr Gln His Leu Asn Arg Ser Leu Arg
275 280 285

Gln Gly Arg Glu Leu Asp Ala Gly Gln Ala Leu Ile Asp Arg Gly Met
290 295 300

Ser Ala Ala Phe Glu Lys Ser Gly Pro Ala Glu Gln Val Val Lys Thr
305 310 315 320

Phe Arg Gly Thr Gln Gly Arg Asp Ala Phe Glu Ala Val Lys Glu Gly
325 330 335

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Gln Val Gly His Asp Ala Gly Tyr Leu Ser Thr Ser Arg Asp Pro Gly
 340 345 350

Val Ala Arg Ser Phe Ala Gly Gln Gly Thr Ile Thr Thr Leu Phe Gly
 355 360 365

Arg Ser Gly Ile Asp Val Ser Glu Ile Ser Ile Glu Gly Asp Glu Gln
 370 375 380

Glu Ile Leu Tyr Asp Lys Gly Thr Asp Met Arg Val Leu Leu Ser Ala
 385 390 395 400

Lys Asp Gly Gln Gly Val Thr Arg Arg Val Leu Glu Glu Ala Thr Leu
 405 410 415

Gly Glu Arg Ser Gly His Gly Glu Gly Leu Leu Asp Ala Leu Asp Leu
 420 425 430

Ala Thr Gly Thr Asp Arg Ser Gly Lys Pro Gln Glu Gln Asp Leu Arg
 435 440 445

Leu Arg Met Arg Gly Leu Asp Leu Ala
 450 455

<210> 17

<211> 322

<212> PRT

<213> NP_047619 Yop targeted effector [Yersinia pestis] YopT

<400> 17

Met Asn Ser Ile His Gly His Tyr His Ile Gln Leu Ser Asn Tyr Ser
 1 5 10 15

Ala Gly Glu Asn Leu Gln Ser Ala Thr Leu Thr Glu Gly Val Ile Gly
 20 25 30

Ala His Arg Val Lys Val Glu Thr Ala Leu Ser His Ser Asn Leu Gln
 35 40 45

Lys Lys Leu Ser Ala Thr Ile Lys His Asn Gln Ser Gly Arg Ser Met
 50 55 60

Leu Asp Arg Lys Leu Thr Ser Asp Gly Lys Ala Asn Gln Arg Ser Ser
 65 70 75 80

Phe Thr Phe Ser Met Ile Met Tyr Arg Met Ile His Phe Val Leu Ser

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85 90 95
 Thr Arg Val Pro Ala Val Arg Glu Ser Val Ala Asn Tyr Gly Gly Asn
 100 105 110
 Ile Asn Phe Lys Phe Ala Gln Thr Lys Gly Ala Phe Leu His Lys Ile
 115 120 125
 Ile Lys His Ser Asp Thr Ala Ser Gly Val Cys Glu Ala Leu Cys Ala
 130 135 140
 His Trp Ile Arg Ser His Ala Gln Gly Gln Ser Leu Phe Asp Gln Leu
 145 150 155 160
 Tyr Val Gly Gly Arg Lys Gly Lys Phe Gln Ile Asp Thr Leu Tyr Ser
 165 170 175
 Ile Lys Gln Leu Gln Ile Asp Gly Cys Lys Ala Asp Val Asp Gln Asp
 180 185 190
 Glu Val Thr Leu Asp Trp Phe Lys Lys Asn Gly Ile Ser Glu Arg Met
 195 200 205
 Ile Glu Arg His Cys Leu Leu Arg Pro Val Asp Val Thr Gly Thr Thr
 210 215 220
 Glu Ser Glu Gly Leu Asp Gln Leu Leu Asn Ala Ile Leu Asp Thr His
 225 230 235 240
 Gly Ile Gly Tyr Gly Tyr Lys Lys Ile His Leu Ser Gly Gln Met Ser
 245 250 255
 Ala His Ala Ile Ala Ala Tyr Val Asn Glu Lys Ser Gly Val Thr Phe
 260 265 270
 Phe Asp Pro Asn Phe Gly Glu Phe His Phe Ser Asp Lys Glu Lys Phe
 275 280 285
 Arg Lys Trp Phe Thr Asn Ser Phe Trp Gly Asn Ser Met Tyr His Tyr
 290 295 300
 Pro Leu Gly Val Gly Gln Arg Phe Arg Val Leu Thr Phe Asp Ser Lys
 305 310 315 320
 Glu Val

<210> 18

<211> 729

<212> PRT

<213> NP_052380 protein kinase YopO [Yersinia enterocolitica]

<400> 18

Met Lys Ile Met Gly Thr Met Pro Pro Ser Ile Ser Leu Ala Lys Ala
 1 5 10 15

His Glu Arg Ile Ser Gln His Trp Gln Asn Pro Val Gly Glu Leu Asn
 20 25 30

Ile Gly Gly Lys Arg Tyr Arg Ile Ile Asp Asn Gln Val Leu Arg Leu
 35 40 45

Asn Pro His Ser Gly Phe Ser Leu Phe Arg Glu Gly Val Gly Lys Ile
 50 55 60

Phe Ser Gly Lys Met Phe Asn Phe Ser Ile Ala Arg Asn Leu Thr Glu
 65 70 75 80

Thr Leu His Ala Ala Gln Lys Thr Thr Ser Gln Glu Leu Arg Ser Asp
 85 90 95

Ile Pro Asn Ala Leu Ser Asn Leu Phe Gly Ala Lys Pro Gln Thr Glu
 100 105 110

Leu Pro Leu Gly Trp Lys Gly Lys Pro Leu Ser Gly Ala Pro Asp Leu
 115 120 125

Glu Gly Met Arg Val Ala Glu Thr Asp Lys Phe Ala Glu Gly Glu Ser
 130 135 140

His Ile Ser Ile Ile Glu Thr Lys Asp Asn Gln Arg Leu Val Ala Lys
 145 150 155 160

Ile Glu Arg Ser Ile Ala Glu Gly His Leu Phe Ala Glu Leu Glu Ala
 165 170 175

Tyr Lys His Ile Tyr Lys Thr Ala Gly Lys His Pro Asn Leu Ala Asn
 180 185 190

Val His Gly Met Ala Val Val Pro Tyr Gly Asn Arg Lys Glu Glu Ala
 195 200 205

Leu Leu Met Asp Glu Val Asp Gly Trp Arg Cys Ser Asp Thr Leu Arg
 210 215 220

Ser Leu Ala Asp Ser Trp Lys Gln Gly Lys Ile Asn Ser Glu Ala Tyr
 225 230 235 240

Trp Gly Thr Ile Lys Phe Ile Ala His Arg Leu Leu Asp Val Thr Asn
 245 250 255

His Leu Ala Lys Ala Gly Ile Val His Asn Asp Ile Lys Pro Gly Asn
 260 265 270

Val Val Phe Asp Arg Ala Ser Gly Glu Pro Val Val Ile Asp Leu Gly
 275 280 285

Leu His Ser Arg Ser Gly Glu Gln Pro Lys Gly Phe Thr Glu Ser Phe
 290 295 300

Lys Ala Pro Glu Leu Gly Val Gly Asn Leu Gly Ala Ser Glu Lys Ser
 305 310 315 320

Asp Val Phe Leu Val Val Ser Thr Leu Leu His Gly Ile Glu Gly Phe
 325 330 335

Glu Lys Asp Pro Glu Ile Lys Pro Asn Gln Gly Leu Arg Phe Ile Thr
 340 345 350

Ser Glu Pro Ala His Val Met Asp Glu Asn Gly Tyr Pro Ile His Arg
 355 360 365

Pro Gly Ile Ala Gly Val Glu Thr Ala Tyr Thr Arg Phe Ile Thr Asp
 370 375 380

Ile Leu Gly Val Ser Ala Asp Ser Arg Pro Asp Ser Asn Glu Ala Arg
 385 390 395 400

Leu His Glu Phe Leu Ser Asp Gly Thr Ile Asp Glu Glu Ser Ala Lys
 405 410 415

Gln Ile Leu Lys Asp Thr Leu Thr Gly Glu Met Ser Pro Leu Ser Thr
 420 425 430

Asp Val Arg Arg Ile Thr Pro Lys Lys Leu Arg Glu Leu Ser Asp Leu
 435 440 445

Leu Arg Thr His Leu Ser Ser Ala Ala Thr Lys Gln Leu Asp Met Gly
 450 455 460

Val Val Leu Ser Asp Leu Asp Thr Met Leu Val Thr Leu Asp Lys Ala
 465 470 475 480

Glu Arg Glu Gly Gly Val Asp Lys Asp Gln Leu Lys Ser Phe Asn Ser
 485 490 495

Leu Ile Leu Lys Thr Tyr Ser Val Ile Glu Asp Tyr Val Lys Gly Arg

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500	505	510
Glu Gly Asp Thr Lys Ser Ser Ser Ala Glu Val Ser Pro Tyr His Arg 515 520 525		
Ser Asn Phe Met Leu Ser Ile Ala Glu Pro Ser Leu Gln Arg Ile Gln 530 535 540		
Lys His Leu Asp Gln Thr His Ser Phe Ser Asp Ile Gly Ser Leu Val 545 550 555 560		
Arg Ala His Lys His Leu Glu Thr Leu Leu Glu Val Leu Val Thr Leu 565 570 575		
Ser Pro Gln Gly Gln Pro Val Ser Ser Glu Thr Tyr Ser Phe Leu Asn 580 585 590		
Arg Leu Ala Glu Ala Lys Val Thr Leu Ser Gln Gln Leu Asp Thr Leu 595 600 605		
Gln Gln Gln Gln Glu Ser Ala Lys Ala Gln Leu Ser Ile Leu Ile Asn 610 615 620		
Arg Ser Gly Ser Trp Ala Asp Val Ala Arg Gln Ser Leu Gln Arg Phe 625 630 635 640		
Asp Ser Thr Arg Pro Val Val Lys Phe Gly Thr Glu Gln Tyr Thr Ala 645 650 655		
Ile His Arg Gln Met Met Ala Ala His Ala Ala Ile Thr Leu Gln Glu 660 665 670		
Val Ser Glu Phe Thr Asp Asp Met Arg Asn Phe Thr Ala Asp Ser Ile 675 680 685		
Pro Leu Leu Ile Arg Leu Gly Arg Ser Ser Leu Ile Asp Glu His Leu 690 695 700		
Val Glu Gln Arg Glu Lys Leu Arg Glu Leu Thr Thr Ile Ala Glu Arg 705 710 715 720		
Leu Asn Arg Leu Glu Arg Glu Trp Met 725		

<210> 19

<211> 129

<212> PRT

<213> AAF82095 outer protein AvrA [Salmonella enterica subsp. enterica

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serovar Dublin]

<400> 19

Val	Met	Asp	Gly	Lys	Thr	Ser	Val	Ile	Leu	Phe	Glu	Pro	Ala	Ala	Cys
1				5					10					15	

Ser	Ala	Phe	Gly	Pro	Ala	Leu	Leu	Ala	Leu	Arg	Thr	Lys	Ala	Ala	Leu
			20					25					30		

Glu	Arg	Glu	Gln	Leu	Pro	Asp	Cys	Tyr	Phe	Ala	Met	Val	Glu	Leu	Asp
		35					40					45			

Ile	Gln	Arg	Ser	Ser	Ser	Glu	Cys	Gly	Ile	Phe	Ser	Leu	Ala	Leu	Ala
	50					55					60				

Lys	Lys	Leu	Gln	Leu	Glu	Phe	Met	Asn	Leu	Val	Lys	Ile	His	Glu	Asp
65				70						75				80	

Asn	Ile	Cys	Glu	Arg	Leu	Cys	Gly	Glu	Glu	Pro	Phe	Leu	Pro	Ser	Asp
			85					90						95	

Lys	Ala	Asp	Arg	Tyr	Leu	Pro	Val	Ser	Phe	Tyr	Lys	His	Thr	Gln	Gly
			100					105					110		

Val	Gln	Arg	Leu	Asn	Glu	Tyr	Val	Glu	Ala	Asn	Pro	Ala	Ala	Gly	Ser
	115						120					125			

Ser

<210> 20

<211> 133

<212> PRT

<213> AAC44300 SpiC [Salmonella typhimurium]

<400> 20

Met	Ser	Glu	Glu	Gly	Phe	Met	Leu	Ala	Val	Leu	Lys	Gly	Ile	Pro	Leu
1				5					10					15	

Ile	Gln	Asp	Ile	Arg	Ala	Glu	Gly	Asn	Ser	Arg	Ser	Trp	Ile	Met	Thr
		20					25						30		

Ile	Asp	Gly	His	Pro	Ala	Arg	Gly	Glu	Ile	Phe	Ser	Glu	Ala	Phe	Ser
		35					40					45			

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Ile Ser Leu Phe Leu Asn Asp Leu Glu Ser Leu Pro Lys Pro Cys Leu
 50 55 60

Ala Tyr Val Thr Leu Leu Leu Ala Ala His Pro Asp Val His Asp Tyr
 65 70 75 80

Ala Ile Gln Leu Thr Ala Asp Gly Gly Trp Leu Asn Gly Tyr Tyr Thr
 85 90 95

Thr Ser Ser Ser Ser Glu Leu Ile Ala Ile Glu Ile Glu Lys His Leu
 100 105 110

Ala Leu Thr Cys Ile Leu Lys Asn Val Ile Arg Asn His His Lys Leu
 115 120 125

Tyr Ser Gly Gly Val
 130

<210> 21

<211> 1212

<212> PRT

<213> Protein sequence for SigD with the first 29 codons removed,
 thrombin linker, diphtheria translocation domain, TeNT-HC

<400> 21

Met Gln Ile Leu Ser Gly Gln Gly Lys Ala Pro Ala Lys Ala Pro Asp
 1 5 10 15

Ala Arg Pro Glu Ile Ile Val Leu Arg Glu Pro Gly Ala Thr Trp Gly
 20 25 30

Asn Tyr Leu Gln His Gln Lys Ala Ser Asn His Ser Leu His Asn Leu
 35 40 45

Tyr Asn Leu Gln Arg Asp Leu Leu Thr Val Ala Ala Thr Val Leu Gly
 50 55 60

Lys Gln Asp Pro Val Leu Thr Ser Met Ala Asn Gln Met Glu Leu Ala
 65 70 75 80

Lys Val Lys Ala Asp Arg Pro Ala Thr Lys Gln Glu Glu Ala Ala Ala
 85 90 95

Lys Ala Leu Lys Lys Asn Leu Ile Glu Leu Ile Ala Ala Arg Thr Gln
 100 105 110

Gln Gln Asp Gly Leu Pro Ala Lys Glu Ala His Arg Phe Ala Ala Val

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115		120		125
Ala Phe Arg Asp Ala Gln Val Lys Gln Leu Asn Asn Gln Pro Trp Gln				
130		135		140
Thr Ile Lys Asn Thr Leu Thr His Asn Gly His His Tyr Thr Asn Thr				
145		150		155
Gln Leu Pro Ala Ala Glu Met Lys Ile Gly Ala Lys Asp Ile Phe Pro				
	165		170	175
Ser Ala Tyr Glu Gly Lys Gly Val Cys Ser Trp Asp Thr Lys Asn Ile				
	180		185	190
His His Ala Asn Asn Leu Trp Met Ser Thr Val Ser Val His Glu Asp				
	195		200	205
Gly Lys Asp Lys Thr Leu Phe Phe Asp Gly Ile Arg His Gly Val Leu				
	210		215	220
Ser Pro Tyr His Glu Lys Asp Pro Leu Leu Arg His Val Gly Ala Glu				
	225		230	235
Asn Lys Ala Lys Glu Val Leu Thr Ala Ala Leu Phe Ser Lys Pro Glu				
	245		250	255
Leu Leu Asn Lys Ala Leu Ala Gly Glu Ala Val Ser Leu Lys Leu Val				
	260		265	270
Ser Val Gly Leu Leu Thr Ala Ser Asn Ile Phe Gly Lys Glu Gly Thr				
	275		280	285
Met Val Glu Asp Gln Met Arg Ala Trp Gln Ser Leu Thr Gln Pro Gly				
	290		295	300
Lys Met Ile His Leu Lys Ile Arg Asn Lys Asp Gly Asp Leu Gln Thr				
	305		310	315
Val Lys Ile Lys Pro Asp Val Val Ala Ala Phe Asn Val Gly Val Asn				
	325		330	335
Glu Leu Ala Leu Lys Leu Gly Phe Gly Leu Lys Ala Ser Asp Ser Tyr				
	340		345	350
Asn Ala Glu Ala Leu His Gln Leu Leu Gly Asn Asp Leu Arg Pro Glu				
	355		360	365
Ala Arg Pro Gly Gly Trp Val Gly Glu Trp Leu Ala Gln Tyr Pro Asp				
	370		375	380

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Asn Tyr Glu Val Val Asn Thr Leu Ala Arg Gln Ile Lys Asp Ile Trp
 385 390 395 400

Lys Asn Asn Gln His His Lys Asp Gly Gly Glu Pro Tyr Lys Leu Ala
 405 410 415

Gln Arg Leu Ala Met Leu Ala His Glu Ile Asp Ala Val Pro Ala Trp
 420 425 430

Asn Cys Lys Ser Gly Lys Asp Arg Thr Gly Met Met Asp Ser Glu Ile
 435 440 445

Lys Gly Glu Ile Ile Ser Leu His Gln Thr His Met Leu Ser Ala Pro
 450 455 460

Gly Ser Leu Pro Asp Ser Gly Gly Gln Lys Ile Phe Gln Lys Val Leu
 465 470 475 480

Leu Asn Ser Gly Asn Leu Glu Ile Gln Lys Gln Asn Thr Gly Gly Ala
 485 490 495

Gly Asn Lys Val Met Lys Asn Leu Ser Pro Glu Val Leu Asn Leu Ser
 500 505 510

Tyr Gln Lys Arg Val Gly Asp Glu Asn Ile Trp Gln Ser Val Lys Gly
 515 520 525

Ile Ser Ser Leu Ile Thr Ser Arg Ser Cys Gly Leu Val Pro Arg Gly
 530 535 540

Ser Gly Pro Gly Ser Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu
 545 550 555 560

Asp Trp Asp Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu
 565 570 575

Lys Glu His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys
 580 585 590

Thr Val Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
 595 600 605

Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly
 610 615 620

Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn
 625 630 635 640

Val Ala Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr
 645 650 655

Thr Ala Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile
660 665 670

Ala Asp Gly Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser
675 680 685

Ile Ala Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly
690 695 700

Glu Leu Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
705 710 715 720

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Ser Ala Tyr
725 730 735

Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val
740 745 750

Ser Trp Asn Thr Val Arg Ser Lys Asn Leu Asp Cys Trp Val Asp Asn
755 760 765

Glu Glu Asp Ile Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu
770 775 780

Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser
785 790 795 800

Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys
805 810 815

Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys
820 825 830

Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser
835 840 845

Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr
850 855 860

Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu
865 870 875 880

Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile
885 890 895

Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg
900 905 910

Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe

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915	920	925
Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn 930 935 940		
Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg 945 950 955 960		
Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn 965 970 975		
Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn 980 985 990		
Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe 995 1000 1005		
Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr 1010 1015 1020		
Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val Gln Leu Lys 1025 1030 1035		
Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser Tyr Thr 1040 1045 1050		
Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly Leu 1055 1060 1065		
Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn Glu Ile Asp Ser 1070 1075 1080		
Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val Ser Tyr Asn 1085 1090 1095		
Asn Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe 1100 1105 1110		
Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly 1115 1120 1125		
Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu 1130 1135 1140		
Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala 1145 1150 1155		
Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp 1160 1165 1170		

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Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His
 1175 1180 1185

Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr
 1190 1195 1200

Asp Glu Gly Trp Thr Asn Asp Leu Gln
 1205 1210

<210> 22

<211> 1212

<212> PRT

<213> Protein sequence for SigD with the first 29 codons removed,
 factor Xa linker, diphtheria translocation domain, TeNT-HC

<400> 22

Met Gln Ile Leu Ser Gly Gln Gly Lys Ala Pro Ala Lys Ala Pro Asp
 1 5 10 15

Ala Arg Pro Glu Ile Ile Val Leu Arg Glu Pro Gly Ala Thr Trp Gly
 20 25 30

Asn Tyr Leu Gln His Gln Lys Ala Ser Asn His Ser Leu His Asn Leu
 35 40 45

Tyr Asn Leu Gln Arg Asp Leu Leu Thr Val Ala Ala Thr Val Leu Gly
 50 55 60

Lys Gln Asp Pro Val Leu Thr Ser Met Ala Asn Gln Met Glu Leu Ala
 65 70 75 80

Lys Val Lys Ala Asp Arg Pro Ala Thr Lys Gln Glu Glu Ala Ala Ala
 85 90 95

Lys Ala Leu Lys Lys Asn Leu Ile Glu Leu Ile Ala Ala Arg Thr Gln
 100 105 110

Gln Gln Asp Gly Leu Pro Ala Lys Glu Ala His Arg Phe Ala Ala Val
 115 120 125

Ala Phe Arg Asp Ala Gln Val Lys Gln Leu Asn Asn Gln Pro Trp Gln
 130 135 140

Thr Ile Lys Asn Thr Leu Thr His Asn Gly His His Tyr Thr Asn Thr
 145 150 155 160

Gln Leu Pro Ala Ala Glu Met Lys Ile Gly Ala Lys Asp Ile Phe Pro

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	165		170		175
Ser Ala Tyr	Glu Gly Lys Gly Val	Cys Ser Trp Asp Thr	Lys Asn Ile		
	180	185	190		
His His Ala	Asn Asn Leu Trp Met	Ser Thr Val Ser Val	His Glu Asp		
	195	200	205		
Gly Lys Asp	Lys Thr Leu Phe Phe Asp	Gly Ile Arg His Gly Val Leu			
	210	215	220		
Ser Pro Tyr	His Glu Lys Asp Pro Leu Leu	Arg His Val Gly Ala Glu			
	225	230	235	240	
Asn Lys Ala	Lys Glu Val Leu Thr Ala Ala	Leu Phe Ser Lys Pro Glu			
	245	250	255		
Leu Leu Asn	Lys Ala Leu Ala Gly Glu Ala Val Ser Leu Lys Leu Val				
	260	265	270		
Ser Val Gly	Leu Leu Thr Ala Ser Asn Ile Phe Gly Lys Glu Gly Thr				
	275	280	285		
Met Val Glu	Asp Gln Met Arg Ala Trp Gln Ser Leu Thr Gln Pro Gly				
	290	295	300		
Lys Met Ile	His Leu Lys Ile Arg Asn Lys Asp Gly Asp Leu Gln Thr				
	305	310	315	320	
Val Lys Ile	Lys Pro Asp Val Val Ala Ala Phe Asn Val Gly Val Asn				
	325	330	335		
Glu Leu Ala	Leu Lys Leu Gly Phe Gly Leu Lys Ala Ser Asp Ser Tyr				
	340	345	350		
Asn Ala Glu	Ala Leu His Gln Leu Leu Gly Asn Asp Leu Arg Pro Glu				
	355	360	365		
Ala Arg Pro	Gly Gly Trp Val Gly Glu Trp Leu Ala Gln Tyr Pro Asp				
	370	375	380		
Asn Tyr Glu	Val Val Asn Thr Leu Ala Arg Gln Ile Lys Asp Ile Trp				
	385	390	395	400	
Lys Asn Asn	Gln His His Lys Asp Gly Gly Glu Pro Tyr Lys Leu Ala				
	405	410	415		
Gln Arg Leu	Ala Met Leu Ala His Glu Ile Asp Ala Val Pro Ala Trp				
	420	425	430		

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Asn Cys Lys Ser Gly Lys Asp Arg Thr Gly Met Met Asp Ser Glu Ile
 435 440 445

Lys Gly Glu Ile Ile Ser Leu His Gln Thr His Met Leu Ser Ala Pro
 450 455 460

Gly Ser Leu Pro Asp Ser Gly Gly Gln Lys Ile Phe Gln Lys Val Leu
 465 470 475 480

Leu Asn Ser Gly Asn Leu Glu Ile Gln Lys Gln Asn Thr Gly Gly Ala
 485 490 495

Gly Asn Lys Val Met Lys Asn Leu Ser Pro Glu Val Leu Asn Leu Ser
 500 505 510

Tyr Gln Lys Arg Val Gly Asp Glu Asn Ile Trp Gln Ser Val Lys Gly
 515 520 525

Ile Ser Ser Leu Ile Thr Ser Arg Ser Cys Gly Ile Glu Gly Arg Ala
 530 535 540

Pro Gly Pro Gly Ser Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu
 545 550 555 560

Asp Trp Asp Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu
 565 570 575

Lys Glu His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys
 580 585 590

Thr Val Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
 595 600 605

Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly
 610 615 620

Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn
 625 630 635 640

Val Ala Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr
 645 650 655

Thr Ala Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile
 660 665 670

Ala Asp Gly Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser
 675 680 685

Ile Ala Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly
 690 695 700

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Glu Leu Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
705 710 715 720

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Ser Ala Tyr
725 730 735

Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val
740 745 750

Ser Trp Asn Thr Val Arg Ser Lys Asn Leu Asp Cys Trp Val Asp Asn
755 760 765

Glu Glu Asp Ile Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu
770 775 780

Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser
785 790 795 800

Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys
805 810 815

Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys
820 825 830

Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser
835 840 845

Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr
850 855 860

Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu
865 870 875 880

Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile
885 890 895

Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg
900 905 910

Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe
915 920 925

Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn
930 935 940

Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg
945 950 955 960

Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn

965

970

975

Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn
 980 985 990

Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe
 995 1000 1005

Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr
 1010 1015 1020

Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val Gln Leu Lys
 1025 1030 1035

Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser Tyr Thr
 1040 1045 1050

Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly Leu
 1055 1060 1065

Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn Glu Ile Asp Ser
 1070 1075 1080

Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val Ser Tyr Asn
 1085 1090 1095

Asn Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe
 1100 1105 1110

Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly
 1115 1120 1125

Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu
 1130 1135 1140

Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala
 1145 1150 1155

Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp
 1160 1165 1170

Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His
 1175 1180 1185

Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr
 1190 1195 1200

Asp Glu Gly Trp Thr Asn Asp Leu Gln
 1205 1210

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<210> 23

<211> 1192

<212> PRT

<213> Protein sequence for SigD with the first 29 codons removed,
thrombin linker, diphtheria toxin translocation domain, with BoNT/F-HC

<400> 23

Met Gln Ile Leu Ser Gly Gln Gly Lys Ala Pro Ala Lys Ala Pro Asp
1 5 10 15

Ala Arg Pro Glu Ile Ile Val Leu Arg Glu Pro Gly Ala Thr Trp Gly
20 25 30

Asn Tyr Leu Gln His Gln Lys Ala Ser Asn His Ser Leu His Asn Leu
35 40 45

Tyr Asn Leu Gln Arg Asp Leu Leu Thr Val Ala Ala Thr Val Leu Gly
50 55 60

Lys Gln Asp Pro Val Leu Thr Ser Met Ala Asn Gln Met Glu Leu Ala
65 70 75 80

Lys Val Lys Ala Asp Arg Pro Ala Thr Lys Gln Glu Glu Ala Ala Ala
85 90 95

Lys Ala Leu Lys Lys Asn Leu Ile Glu Leu Ile Ala Ala Arg Thr Gln
100 105 110

Gln Gln Asp Gly Leu Pro Ala Lys Glu Ala His Arg Phe Ala Ala Val
115 120 125

Ala Phe Arg Asp Ala Gln Val Lys Gln Leu Asn Asn Gln Pro Trp Gln
130 135 140

Thr Ile Lys Asn Thr Leu Thr His Asn Gly His His Tyr Thr Asn Thr
145 150 155 160

Gln Leu Pro Ala Ala Glu Met Lys Ile Gly Ala Lys Asp Ile Phe Pro
165 170 175

Ser Ala Tyr Glu Gly Lys Gly Val Cys Ser Trp Asp Thr Lys Asn Ile
180 185 190

His His Ala Asn Asn Leu Trp Met Ser Thr Val Ser Val His Glu Asp
195 200 205

Gly Lys Asp Lys Thr Leu Phe Phe Asp Gly Ile Arg His Gly Val Leu

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210	215	220
Ser Pro Tyr His Glu Lys Asp Pro Leu Leu Arg His Val Gly Ala Glu		
225	230	235 240
Asn Lys Ala Lys Glu Val Leu Thr Ala Ala Leu Phe Ser Lys Pro Glu		
	245	250 255
Leu Leu Asn Lys Ala Leu Ala Gly Glu Ala Val Ser Leu Lys Leu Val		
	260	265 270
Ser Val Gly Leu Leu Thr Ala Ser Asn Ile Phe Gly Lys Glu Gly Thr		
	275	280 285
Met Val Glu Asp Gln Met Arg Ala Trp Gln Ser Leu Thr Gln Pro Gly		
	290	295 300
Lys Met Ile His Leu Lys Ile Arg Asn Lys Asp Gly Asp Leu Gln Thr		
305	310	315 320
Val Lys Ile Lys Pro Asp Val Val Ala Ala Phe Asn Val Gly Val Asn		
	325	330 335
Glu Leu Ala Leu Lys Leu Gly Phe Gly Leu Lys Ala Ser Asp Ser Tyr		
	340	345 350
Asn Ala Glu Ala Leu His Gln Leu Leu Gly Asn Asp Leu Arg Pro Glu		
	355	360 365
Ala Arg Pro Gly Gly Trp Val Gly Glu Trp Leu Ala Gln Tyr Pro Asp		
	370	375 380
Asn Tyr Glu Val Val Asn Thr Leu Ala Arg Gln Ile Lys Asp Ile Trp		
385	390	395 400
Lys Asn Asn Gln His His Lys Asp Gly Gly Glu Pro Tyr Lys Leu Ala		
	405	410 415
Gln Arg Leu Ala Met Leu Ala His Glu Ile Asp Ala Val Pro Ala Trp		
	420	425 430
Asn Cys Lys Ser Gly Lys Asp Arg Thr Gly Met Met Asp Ser Glu Ile		
	435	440 445
Lys Gly Glu Ile Ile Ser Leu His Gln Thr His Met Leu Ser Ala Pro		
	450	455 460
Gly Ser Leu Pro Asp Ser Gly Gly Gln Lys Ile Phe Gln Lys Val Leu		
465	470	475 480

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Leu Asn Ser Gly Asn Leu Glu Ile Gln Lys Gln Asn Thr Gly Gly Ala
485 490 495

Gly Asn Lys Val Met Lys Asn Leu Ser Pro Glu Val Leu Asn Leu Ser
500 505 510

Tyr Gln Lys Arg Val Gly Asp Glu Asn Ile Trp Gln Ser Val Lys Gly
515 520 525

Ile Ser Ser Leu Ile Thr Ser Arg Ser Cys Gly Leu Val Pro Arg Gly
530 535 540

Ser Gly Pro Gly Ser Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu
545 550 555 560

Asp Trp Asp Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu
565 570 575

Lys Glu His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys
580 585 590

Thr Val Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
595 600 605

Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly
610 615 620

Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn
625 630 635 640

Val Ala Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr
645 650 655

Thr Ala Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile
660 665 670

Ala Asp Gly Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser
675 680 685

Ile Ala Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly
690 695 700

Glu Leu Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
705 710 715 720

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Ser Ala Tyr
725 730 735

Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val
740 745 750

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Ser Trp Asn Thr Val Arg Ser Thr Met Ser Tyr Thr Asn Asp Lys Ile
755 760 765

Leu Ile Leu Tyr Phe Asn Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser
770 775 780

Ile Leu Asp Met Arg Tyr Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly
785 790 795 800

Tyr Gly Ser Asn Ile Ser Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr
805 810 815

Asn Arg Asn Gln Phe Gly Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn
820 825 830

Ile Ala Gln Asn Asn Asp Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe
835 840 845

Ser Ile Ser Phe Trp Val Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn
850 855 860

Leu Asn Asn Glu Tyr Thr Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser
865 870 875 880

Gly Trp Lys Ile Ser Leu Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln
885 890 895

Asp Thr Ala Gly Asn Asn Gln Lys Leu Val Phe Asn Tyr Thr Gln Met
900 905 910

Ile Ser Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile Thr
915 920 925

Asn Asn Arg Leu Gly Asn Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile
930 935 940

Asp Glu Lys Ser Ile Ser Asn Leu Gly Asp Ile His Val Ser Asp Asn
945 950 955 960

Ile Leu Phe Lys Ile Val Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile
965 970 975

Arg Tyr Phe Lys Val Phe Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu
980 985 990

Thr Leu Tyr Ser Asp Glu Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp
995 1000 1005

Gly Asn Tyr Leu Leu Tyr Asn Lys Arg Tyr Tyr Leu Leu Asn Leu

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1010 1015 1020
 Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn Ser Asn Phe Leu Asn
 1025 1030 1035
 Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro Asn Ile Phe Ser
 1040 1045 1050
 Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile Arg Lys Asn
 1055 1060 1065
 Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg Lys Asn
 1070 1075 1080
 Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr Arg
 1085 1090 1095
 Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys
 1100 1105 1110
 Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
 1115 1120 1125
 Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn
 1130 1135 1140
 Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
 1145 1150 1155
 Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr
 1160 1165 1170
 Ser Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly
 1175 1180 1185
 Trp Gln Glu Asn
 1190

<210> 24

<211> 1192

<212> PRT

<213> Protein sequence for SigD, factor Xa linker, diphtheria toxin translocation domain, with BoNT/F-HC

<400> 24

Met Gln Ile Leu Ser Gly Gln Gly Lys Ala Pro Ala Lys Ala Pro Asp
 1 5 10 15

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Ala Arg Pro Glu Ile Ile Val Leu Arg Glu Pro Gly Ala Thr Trp Gly
 20 25 30

Asn Tyr Leu Gln His Gln Lys Ala Ser Asn His Ser Leu His Asn Leu
 35 40 45

Tyr Asn Leu Gln Arg Asp Leu Leu Thr Val Ala Ala Thr Val Leu Gly
 50 55 60

Lys Gln Asp Pro Val Leu Thr Ser Met Ala Asn Gln Met Glu Leu Ala
 65 70 75 80

Lys Val Lys Ala Asp Arg Pro Ala Thr Lys Gln Glu Glu Ala Ala Ala
 85 90 95

Lys Ala Leu Lys Lys Asn Leu Ile Glu Leu Ile Ala Ala Arg Thr Gln
 100 105 110

Gln Gln Asp Gly Leu Pro Ala Lys Glu Ala His Arg Phe Ala Ala Val
 115 120 125

Ala Phe Arg Asp Ala Gln Val Lys Gln Leu Asn Asn Gln Pro Trp Gln
 130 135 140

Thr Ile Lys Asn Thr Leu Thr His Asn Gly His His Tyr Thr Asn Thr
 145 150 155 160

Gln Leu Pro Ala Ala Glu Met Lys Ile Gly Ala Lys Asp Ile Phe Pro
 165 170 175

Ser Ala Tyr Glu Gly Lys Gly Val Cys Ser Trp Asp Thr Lys Asn Ile
 180 185 190

His His Ala Asn Asn Leu Trp Met Ser Thr Val Ser Val His Glu Asp
 195 200 205

Gly Lys Asp Lys Thr Leu Phe Phe Asp Gly Ile Arg His Gly Val Leu
 210 215 220

Ser Pro Tyr His Glu Lys Asp Pro Leu Leu Arg His Val Gly Ala Glu
 225 230 235 240

Asn Lys Ala Lys Glu Val Leu Thr Ala Ala Leu Phe Ser Lys Pro Glu
 245 250 255

Leu Leu Asn Lys Ala Leu Ala Gly Glu Ala Val Ser Leu Lys Leu Val
 260 265 270

Ser Val Gly Leu Leu Thr Ala Ser Asn Ile Phe Gly Lys Glu Gly Thr

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275	280	285
Met Val Glu Asp Gln Met Arg Ala Trp Gln Ser Leu Thr Gln Pro Gly 290 295 300		
Lys Met Ile His Leu Lys Ile Arg Asn Lys Asp Gly Asp Leu Gln Thr 305 310 315 320		
Val Lys Ile Lys Pro Asp Val Val Ala Ala Phe Asn Val Gly Val Asn 325 330 335		
Glu Leu Ala Leu Lys Leu Gly Phe Gly Leu Lys Ala Ser Asp Ser Tyr 340 345 350		
Asn Ala Glu Ala Leu His Gln Leu Leu Gly Asn Asp Leu Arg Pro Glu 355 360 365		
Ala Arg Pro Gly Gly Trp Val Gly Glu Trp Leu Ala Gln Tyr Pro Asp 370 375 380		
Asn Tyr Glu Val Val Asn Thr Leu Ala Arg Gln Ile Lys Asp Ile Trp 385 390 395 400		
Lys Asn Asn Gln His His Lys Asp Gly Gly Glu Pro Tyr Lys Leu Ala 405 410 415		
Gln Arg Leu Ala Met Leu Ala His Glu Ile Asp Ala Val Pro Ala Trp 420 425 430		
Asn Cys Lys Ser Gly Lys Asp Arg Thr Gly Met Met Asp Ser Glu Ile 435 440 445		
Lys Gly Glu Ile Ile Ser Leu His Gln Thr His Met Leu Ser Ala Pro 450 455 460		
Gly Ser Leu Pro Asp Ser Gly Gly Gln Lys Ile Phe Gln Lys Val Leu 465 470 475 480		
Leu Asn Ser Gly Asn Leu Glu Ile Gln Lys Gln Asn Thr Gly Gly Ala 485 490 495		
Gly Asn Lys Val Met Lys Asn Leu Ser Pro Glu Val Leu Asn Leu Ser 500 505 510		
Tyr Gln Lys Arg Val Gly Asp Glu Asn Ile Trp Gln Ser Val Lys Gly 515 520 525		
Ile Ser Ser Leu Ile Thr Ser Arg Ser Cys Gly Ile Glu Gly Arg Ala 530 535 540		

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Pro Gly Pro Gly Ser Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu
 545 550 555 560

Asp Trp Asp Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu
 565 570 575

Lys Glu His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys
 580 585 590

Thr Val Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
 595 600 605

Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly
 610 615 620

Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn
 625 630 635 640

Val Ala Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr
 645 650 655

Thr Ala Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile
 660 665 670

Ala Asp Gly Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser
 675 680 685

Ile Ala Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly
 690 695 700

Glu Leu Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
 705 710 715 720

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Ser Ala Tyr
 725 730 735

Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val
 740 745 750

Ser Trp Asn Thr Val Arg Ser Thr Met Ser Tyr Thr Asn Asp Lys Ile
 755 760 765

Leu Ile Leu Tyr Phe Asn Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser
 770 775 780

Ile Leu Asp Met Arg Tyr Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly
 785 790 795 800

Tyr Gly Ser Asn Ile Ser Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr
 805 810 815

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Asn Arg Asn Gln Phe Gly Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn
 820 825 830

Ile Ala Gln Asn Asn Asp Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe
 835 840 845

Ser Ile Ser Phe Trp Val Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn
 850 855 860

Leu Asn Asn Glu Tyr Thr Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser
 865 870 875 880

Gly Trp Lys Ile Ser Leu Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln
 885 890 895

Asp Thr Ala Gly Asn Asn Gln Lys Leu Val Phe Asn Tyr Thr Gln Met
 900 905 910

Ile Ser Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile Thr
 915 920 925

Asn Asn Arg Leu Gly Asn Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile
 930 935 940

Asp Glu Lys Ser Ile Ser Asn Leu Gly Asp Ile His Val Ser Asp Asn
 945 950 955 960

Ile Leu Phe Lys Ile Val Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile
 965 970 975

Arg Tyr Phe Lys Val Phe Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu
 980 985 990

Thr Leu Tyr Ser Asp Glu Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp
 995 1000 1005

Gly Asn Tyr Leu Leu Tyr Asn Lys Arg Tyr Tyr Leu Leu Asn Leu
 1010 1015 1020

Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn Ser Asn Phe Leu Asn
 1025 1030 1035

Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro Asn Ile Phe Ser
 1040 1045 1050

Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile Arg Lys Asn
 1055 1060 1065

Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg Lys Asn

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1070 1075 1080
 Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr Arg
 1085 1090 1095

 Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys
 1100 1105 1110

 Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
 1115 1120 1125

 Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn
 1130 1135 1140

 Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
 1145 1150 1155

 Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr
 1160 1165 1170

 Ser Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly
 1175 1180 1185

 Trp Gln Glu Asn
 1190

 <210> 25
 <211> 999
 <212> PRT
 <213> Protein sequence for YopT, factor Xa linker, diphtheria
 translocation domain, TeNT- HC

 <400> 25
 Met Asn Ser Ile His Gly His Tyr His Ile Gln Leu Ser Asn Tyr Ser
 1 5 10 15

 Ala Gly Glu Asn Leu Gln Ser Ala Thr Leu Thr Glu Gly Val Ile Gly
 20 25 30

 Ala His Arg Val Lys Val Glu Thr Ala Leu Ser His Ser Asn Leu Gln
 35 40 45

 Lys Lys Leu Ser Ala Thr Ile Lys His Asn Gln Ser Gly Arg Ser Met
 50 55 60

 Leu Asp Arg Lys Leu Thr Ser Asp Gly Lys Ala Asn Gln Arg Ser Ser
 65 70 75 80

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Phe Thr Phe Ser Met Ile Met Tyr Arg Met Ile His Phe Val Leu Ser
 85 90 95

Thr Arg Val Pro Ala Val Arg Glu Ser Val Ala Asn Tyr Gly Gly Asn
 100 105 110

Ile Asn Phe Lys Phe Ala Gln Thr Lys Gly Ala Phe Leu His Lys Ile
 115 120 125

Ile Lys His Ser Asp Thr Ala Ser Gly Val Cys Glu Ala Leu Cys Ala
 130 135 140

His Trp Ile Arg Ser His Ala Gln Gly Gln Ser Leu Phe Asp Gln Leu
 145 150 155 160

Tyr Val Gly Gly Arg Lys Gly Lys Phe Gln Ile Asp Thr Leu Tyr Ser
 165 170 175

Ile Lys Gln Leu Gln Ile Asp Gly Cys Lys Ala Asp Val Asp Gln Asp
 180 185 190

Glu Val Thr Leu Asp Trp Phe Lys Lys Asn Gly Ile Ser Glu Arg Met
 195 200 205

Ile Glu Arg His Cys Leu Leu Arg Pro Val Asp Val Thr Gly Thr Thr
 210 215 220

Glu Ser Glu Gly Leu Asp Gln Leu Leu Asn Ala Ile Leu Asp Thr His
 225 230 235 240

Gly Ile Gly Tyr Gly Tyr Lys Lys Ile His Leu Ser Gly Gln Met Ser
 245 250 255

Ala His Ala Ile Ala Ala Tyr Val Asn Glu Lys Ser Gly Val Thr Phe
 260 265 270

Phe Asp Pro Asn Phe Gly Glu Phe His Phe Ser Asp Lys Glu Lys Phe
 275 280 285

Arg Lys Trp Phe Thr Asn Ser Phe Trp Gly Asn Ser Met Tyr His Tyr
 290 295 300

Pro Leu Gly Val Gly Gln Arg Phe Arg Val Leu Thr Phe Asp Ser Lys
 305 310 315 320

Glu Val Arg Ser Cys Gly Ile Glu Gly Arg Ala Pro Gly Pro Gly Ser
 325 330 335

Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile

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340	345	350
Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly Pro 355 360 365		
Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu 370 375 380		
Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu His 385 390 395 400		
Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val Phe 405 410 415		
Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val Ile 420 425 430		
Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser 435 440 445		
Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val 450 455 460		
His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser 465 470 475 480		
Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile 485 490 495		
Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe Gln 500 505 510		
Val Val His Asn Ser Tyr Asn Arg Ser Ala Tyr Ser Pro Gly His Lys 515 520 525		
Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr Val 530 535 540		
Arg Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp 545 550 555 560		
Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp 565 570 575		
Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro 580 585 590		
Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val 595 600 605		

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Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu
 610 615 620

Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
 625 630 635 640

Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr
 645 650 655

Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly
 660 665 670

Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp
 675 680 685

Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys
 690 695 700

Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn
 705 710 715 720

Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly
 725 730 735

Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile
 740 745 750

Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile
 755 760 765

Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu
 770 775 780

Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp
 785 790 795 800

Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala
 805 810 815

Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr
 820 825 830

Leu Thr Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile Tyr Tyr
 835 840 845

Arg Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr Pro
 850 855 860

Asn Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys Leu
 865 870 875 880

Gly Asn Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn
900 905 910

Ala Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg
915 920 925

Asp Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn
930 935 940

Ala Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp
945 950 955 960

Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His Leu
965 970 975

Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp Glu
980 985 990

Gly Trp Thr Asn Asp Leu Gln
995

<210> 26

<211> 979

<212> PRT

<213> Protein sequence for YopT, factor Xa linker, diphtheria toxin translocation domain, with BoNT/F-HC

<400> 26

Met Asn Ser Ile His Gly His Tyr His Ile Gln Leu Ser Asn Tyr Ser
1 5 10 15

Ala Gly Glu Asn Leu Gln Ser Ala Thr Leu Thr Glu Gly Val Ile Gly
20 25 30

Ala His Arg Val Lys Val Glu Thr Ala Leu Ser His Ser Asn Leu Gln
35 40 45

Lys Lys Leu Ser Ala Thr Ile Lys His Asn Gln Ser Gly Arg Ser Met
50 55 60

Leu Asp Arg Lys Leu Thr Ser Asp Gly Lys Ala Asn Gln Arg Ser Ser
65 70 75 80

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Phe Thr Phe Ser Met Ile Met Tyr Arg Met Ile His Phe Val Leu Ser
85 90 95

Thr Arg Val Pro Ala Val Arg Glu Ser Val Ala Asn Tyr Gly Gly Asn
100 105 110

Ile Asn Phe Lys Phe Ala Gln Thr Lys Gly Ala Phe Leu His Lys Ile
115 120 125

Ile Lys His Ser Asp Thr Ala Ser Gly Val Cys Glu Ala Leu Cys Ala
130 135 140

His Trp Ile Arg Ser His Ala Gln Gly Gln Ser Leu Phe Asp Gln Leu
145 150 155 160

Tyr Val Gly Gly Arg Lys Gly Lys Phe Gln Ile Asp Thr Leu Tyr Ser
165 170 175

Ile Lys Gln Leu Gln Ile Asp Gly Cys Lys Ala Asp Val Asp Gln Asp
180 185 190

Glu Val Thr Leu Asp Trp Phe Lys Lys Asn Gly Ile Ser Glu Arg Met
195 200 205

Ile Glu Arg His Cys Leu Leu Arg Pro Val Asp Val Thr Gly Thr Thr
210 215 220

Glu Ser Glu Gly Leu Asp Gln Leu Leu Asn Ala Ile Leu Asp Thr His
225 230 235 240

Gly Ile Gly Tyr Gly Tyr Lys Lys Ile His Leu Ser Gly Gln Met Ser
245 250 255

Ala His Ala Ile Ala Ala Tyr Val Asn Glu Lys Ser Gly Val Thr Phe
260 265 270

Phe Asp Pro Asn Phe Gly Glu Phe His Phe Ser Asp Lys Glu Lys Phe
275 280 285

Arg Lys Trp Phe Thr Asn Ser Phe Trp Gly Asn Ser Met Tyr His Tyr
290 295 300

Pro Leu Gly Val Gly Gln Arg Phe Arg Val Leu Thr Phe Asp Ser Lys
305 310 315 320

Glu Val Arg Ser Cys Gly Ile Glu Gly Arg Ala Pro Gly Pro Gly Ser
325 330 335

Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile
340 345 350

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Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly Pro
 355 360 365

Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu
 370 375 380

Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu His
 385 390 395 400

Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val Phe
 405 410 415

Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val Ile
 420 425 430

Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser
 435 440 445

Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val
 450 455 460

His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser
 465 470 475 480

Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile
 485 490 495

Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe Gln
 500 505 510

Val Val His Asn Ser Tyr Asn Arg Ser Ala Tyr Ser Pro Gly His Lys
 515 520 525

Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr Val
 530 535 540

Arg Ser Thr Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe
 545 550 555 560

Asn Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg
 565 570 575

Tyr Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile
 580 585 590

Ser Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe
 595 600 605

Gly Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn

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610	615	620
Asp Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp 625 630 635 640		
Val Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr 645 650 655		
Thr Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser 660 665 670		
Leu Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn 675 680 685		
Asn Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp 690 695 700		
Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly 705 710 715 720		
Asn Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile 725 730 735		
Ser Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile 740 745 750		
Val Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val 755 760 765		
Phe Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp 770 775 780		
Glu Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu 785 790 795 800		
Tyr Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser 805 810 815		
Ile Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val 820 825 830		
Tyr Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val 835 840 845		
Glu Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp 850 855 860		
Asn Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg 865 870 875 880		

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Asp Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu
 885 890 895

Lys Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly
 900 905 910

Gln Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe
 915 920 925

Gln Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn
 930 935 940

Asn Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr
 945 950 955 960

Ser Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp
 965 970 975

Gln Glu Asn

<210> 27

<211> 810

<212> PRT

<213> Protein sequence for SpiC, thrombin linker, diphtheria
 translocation domain, TeNT-HC

<400> 27

Met Ser Glu Glu Gly Phe Met Leu Ala Val Leu Lys Gly Ile Pro Leu
 1 5 10 15

Ile Gln Asp Ile Arg Ala Glu Gly Asn Ser Arg Ser Trp Ile Met Thr
 20 25 30

Ile Asp Gly His Pro Ala Arg Gly Glu Ile Phe Ser Glu Ala Phe Ser
 35 40 45

Ile Ser Leu Phe Leu Asn Asp Leu Glu Ser Leu Pro Lys Pro Cys Leu
 50 55 60

Ala Tyr Val Thr Leu Leu Leu Ala Ala His Pro Asp Val His Asp Tyr
 65 70 75 80

Ala Ile Gln Leu Thr Ala Asp Gly Gly Trp Leu Asn Gly Tyr Tyr Thr
 85 90 95

Thr Ser Ser Ser Ser Glu Leu Ile Ala Ile Glu Ile Glu Lys His Leu

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100	105	110
Ala Leu Thr Cys Ile Leu Lys	Asn Val Ile Arg Asn His His Lys Leu	
115	120	125
Tyr Ser Gly Gly Val Arg Ser Cys Gly Leu Val Pro Arg Gly Ser Gly		
130	135	140
Pro Gly Ser Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp		
145	150	155
Asp Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu		
	165	170
His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val		
	180	185
Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala		
	195	200
Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn		
	210	215
Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala		
225	230	235
Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala		
	245	250
Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp		
	260	265
Gly Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala		
	275	280
Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu		
	290	295
Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn		
305	310	315
Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Ser Ala Tyr Ser Pro		
	325	330
Gly His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp		
	340	345
Asn Thr Val Arg Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu		
	355	360
		365

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Asp Ile Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile
 370 375 380

Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile
 385 390 395 400

Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile
 405 410 415

His Leu Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met
 420 425 430

Asp Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp
 435 440 445

Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr
 450 455 460

Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile
 465 470 475 480

Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr
 485 490 495

Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu
 500 505 510

Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr
 515 520 525

Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val
 530 535 540

Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp
 545 550 555 560

Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr
 565 570 575

Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys
 580 585 590

Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg
 595 600 605

Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile
 610 615 620

Pro Val Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp
 625 630 635 640

Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg
660 665 670

Tyr Thr Pro Asn Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe
675 680 685

Ile Lys Leu Tyr Val Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr
690 695 700

Pro Lys Asp Gly Asn Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val
705 710 715 720

Gly Tyr Asn Ala Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val
725 730 735

Lys Leu Arg Asp Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp
740 745 750

Asp Lys Asn Ala Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile
755 760 765

Gly Asn Asp Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe
770 775 780

Asn His Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro
785 790 795 800

Thr Asp Glu Gly Trp Thr Asn Asp Leu Gln
805 810

<210> 28

<211> 810

<212> PRT

<213> Protein sequence for SpiC, factor Xa linker, diphtheria translocation domain, TeNT- HC

<400> 28

Met Ser Glu Glu Gly Phe Met Leu Ala Val Leu Lys Gly Ile Pro Leu
1 5 10 15

Ile Gln Asp Ile Arg Ala Glu Gly Asn Ser Arg Ser Trp Ile Met Thr
20 25 30

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Ile Asp Gly His Pro Ala Arg Gly Glu Ile Phe Ser Glu Ala Phe Ser
 35 40 45

Ile Ser Leu Phe Leu Asn Asp Leu Glu Ser Leu Pro Lys Pro Cys Leu
 50 55 60

Ala Tyr Val Thr Leu Leu Leu Ala Ala His Pro Asp Val His Asp Tyr
 65 70 75 80

Ala Ile Gln Leu Thr Ala Asp Gly Gly Trp Leu Asn Gly Tyr Tyr Thr
 85 90 95

Thr Ser Ser Ser Ser Glu Leu Ile Ala Ile Glu Ile Glu Lys His Leu
 100 105 110

Ala Leu Thr Cys Ile Leu Lys Asn Val Ile Arg Asn His His Lys Leu
 115 120 125

Tyr Ser Gly Gly Val Arg Ser Cys Gly Ile Glu Gly Arg Ala Pro Gly
 130 135 140

Pro Gly Ser Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp
 145 150 155 160

Asp Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu
 165 170 175

His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val
 180 185 190

Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala
 195 200 205

Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn
 210 215 220

Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala
 225 230 235 240

Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala
 245 250 255

Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp
 260 265 270

Gly Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala
 275 280 285

Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu
 290 295 300

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Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn
305 310 315 320

Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Ser Ala Tyr Ser Pro
325 330 335

Gly His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp
340 345 350

Asn Thr Val Arg Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu
355 360 365

Asp Ile Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile
370 375 380

Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile
385 390 395 400

Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile
405 410 415

His Leu Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met
420 425 430

Asp Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp
435 440 445

Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr
450 455 460

Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile
465 470 475 480

Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr
485 490 495

Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu
500 505 510

Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr
515 520 525

Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val
530 535 540

Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp
545 550 555 560

Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr

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565										570					575				
Val	Ser	Ile	Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys	Ala	Leu	Asn	Pro	Lys				
			580					585					590						
Glu	Ile	Glu	Lys	Leu	Tyr	Thr	Ser	Tyr	Leu	Ser	Ile	Thr	Phe	Leu	Arg				
		595					600					605							
Asp	Phe	Trp	Gly	Asn	Pro	Leu	Arg	Tyr	Asp	Thr	Glu	Tyr	Tyr	Leu	Ile				
	610					615					620								
Pro	Val	Ala	Ser	Ser	Ser	Lys	Asp	Val	Gln	Leu	Lys	Asn	Ile	Thr	Asp				
625					630					635					640				
Tyr	Met	Tyr	Leu	Thr	Asn	Ala	Pro	Ser	Tyr	Thr	Asn	Gly	Lys	Leu	Asn				
				645					650						655				
Ile	Tyr	Tyr	Arg	Arg	Leu	Tyr	Asn	Gly	Leu	Lys	Phe	Ile	Ile	Lys	Arg				
			660					665						670					
Tyr	Thr	Pro	Asn	Asn	Glu	Ile	Asp	Ser	Phe	Val	Lys	Ser	Gly	Asp	Phe				
		675					680					685							
Ile	Lys	Leu	Tyr	Val	Ser	Tyr	Asn	Asn	Asn	Glu	His	Ile	Val	Gly	Tyr				
	690					695					700								
Pro	Lys	Asp	Gly	Asn	Ala	Phe	Asn	Asn	Leu	Asp	Arg	Ile	Leu	Arg	Val				
705					710					715					720				
Gly	Tyr	Asn	Ala	Pro	Gly	Ile	Pro	Leu	Tyr	Lys	Lys	Met	Glu	Ala	Val				
				725					730						735				
Lys	Leu	Arg	Asp	Leu	Lys	Thr	Tyr	Ser	Val	Gln	Leu	Lys	Leu	Tyr	Asp				
			740					745						750					
Asp	Lys	Asn	Ala	Ser	Leu	Gly	Leu	Val	Gly	Thr	His	Asn	Gly	Gln	Ile				
		755					760					765							
Gly	Asn	Asp	Pro	Asn	Arg	Asp	Ile	Leu	Ile	Ala	Ser	Asn	Trp	Tyr	Phe				
	770					775						780							
Asn	His	Leu	Lys	Asp	Lys	Ile	Leu	Gly	Cys	Asp	Trp	Tyr	Phe	Val	Pro				
785					790					795					800				
Thr	Asp	Glu	Gly	Trp	Thr	Asn	Asp	Leu	Gln										
				805					810										

<210> 29

<211> 393

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<212> PRT

<213> Protein sequence for SpiC fused to a domain consisting the N-terminal 254 residues from Bacillus anthracis lethal factor capable of interacting with protective antigen

<400> 29

Met Ser Glu Glu Gly Phe Met Leu Ala Val Leu Lys Gly Ile Pro Leu
1 5 10 15

Ile Gln Asp Ile Arg Ala Glu Gly Asn Ser Arg Ser Trp Ile Met Thr
20 25 30

Ile Asp Gly His Pro Ala Arg Gly Glu Ile Phe Ser Glu Ala Phe Ser
35 40 45

Ile Ser Leu Phe Leu Asn Asp Leu Glu Ser Leu Pro Lys Pro Cys Leu
50 55 60

Ala Tyr Val Thr Leu Leu Leu Ala Ala His Pro Asp Val His Asp Tyr
65 70 75 80

Ala Ile Gln Leu Thr Ala Asp Gly Gly Trp Leu Asn Gly Tyr Tyr Thr
85 90 95

Thr Ser Ser Ser Ser Glu Leu Ile Ala Ile Glu Ile Glu Lys His Leu
100 105 110

Ala Leu Thr Cys Ile Leu Lys Asn Val Ile Arg Asn His His Lys Leu
115 120 125

Tyr Ser Gly Gly Val Met Asn Ile Lys Lys Glu Phe Ile Lys Val Ile
130 135 140

Ser Met Ser Cys Leu Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe
145 150 155 160

Ile Pro Leu Val Gln Gly Ala Gly Gly His Gly Asp Val Gly Met His
165 170 175

Val Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu
180 185 190

Glu Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys His
195 200 205

Ile Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala
210 215 220

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Ala Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr
 225 230 235 240

Lys Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys
 245 250 255

His Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp
 260 265 270

Ile Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys
 275 280 285

Glu Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val
 290 295 300

Glu Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile
 305 310 315 320

Leu Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe
 325 330 335

Leu Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln
 340 345 350

Asp Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser
 355 360 365

Val Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala
 370 375 380

Lys Ala Phe Ala Tyr Tyr Ile Glu Pro
 385 390

<210> 30

<211> 764

<212> PRT

<213> Protein sequence of Bacillus anthracis protective antigen

<400> 30

Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile
 1 5 10 15

Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys
 20 25 30

Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu
 35 40 45

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Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
 50 55 60

Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
 65 70 75 80

Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
 85 90 95

Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
 100 105 110

Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
 115 120 125

Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
 130 135 140

Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
 145 150 155 160

Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
 165 170 175

Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
 180 185 190

Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
 195 200 205

Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
 210 215 220

Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
 225 230 235 240

Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
 245 250 255

Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
 260 265 270

Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
 275 280 285

Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
 290 295 300

Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys

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305		310		315		320
Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala						
		325		330		335
Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly						
		340		345		350
Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser						
		355		360		365
Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala						
		370		375		380
Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr						
		385		390		395
Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys						
		405		410		415
Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln						
		420		425		430
Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile						
		435		440		445
Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn						
		450		455		460
Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp						
		465		470		475
Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly						
		485		490		495
Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln						
		500		505		510
Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn						
		515		520		525
Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu						
		530		535		540
Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe						
		545		550		555
Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile						
		565		570		575

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Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
 580 585 590

Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
 595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
 610 615 620

Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
 625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
 645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
 660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
 675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
 690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
 705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
 725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
 740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
 755 760

<210> 31

<211> 431

<212> PRT

<213> Protein sequence of Clostridium botulinum C2 toxin component 1

<400> 31

Met Pro Ile Ile Lys Glu Pro Ile Asp Phe Ile Asn Lys Pro Glu Ser
 1 5 10 15

Glu Ala Gln Lys Trp Gly Lys Glu Glu Glu Lys Arg Trp Phe Thr Lys
 20 25 30

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Leu Asn Asn Leu Glu Glu Val Ala Val Asn Gln Leu Lys Thr Lys Glu
 35 40 45

Asp Lys Thr Lys Ile Asp Asn Phe Ser Thr Asp Ile Leu Phe Ser Ser
 50 55 60

Leu Thr Ala Ile Glu Ile Met Lys Glu Asp Glu Asn Gln Asn Leu Phe
 65 70 75 80

Asp Val Glu Arg Ile Arg Glu Ala Leu Leu Lys Asn Thr Leu Asp Arg
 85 90 95

Glu Val Ile Gly Tyr Val Asn Phe Thr Pro Lys Glu Leu Gly Ile Asn
 100 105 110

Phe Ser Ile Arg Asp Val Glu Leu Asn Arg Asp Ile Ser Asp Glu Ile
 115 120 125

Leu Asp Lys Val Arg Gln Gln Ile Ile Asn Gln Glu Tyr Thr Lys Phe
 130 135 140

Ser Phe Val Ser Leu Gly Leu Asn Asp Asn Ser Ile Asp Glu Ser Ile
 145 150 155 160

Pro Val Ile Val Lys Thr Arg Val Pro Thr Thr Phe Asn Tyr Gly Val
 165 170 175

Leu Asn Asn Lys Glu Thr Val Ser Leu Leu Leu Asn Gln Gly Phe Ser
 180 185 190

Ile Ile Pro Glu Ser Ala Ile Ile Thr Thr Ile Lys Gly Lys Asp Tyr
 195 200 205

Ile Leu Ile Glu Gly Ser Leu Ser Gln Glu Leu Asp Phe Tyr Asn Lys
 210 215 220

Gly Ser Glu Ala Trp Gly Glu Lys Asn Tyr Gly Asp Tyr Val Ser Lys
 225 230 235 240

Leu Ser Gln Glu Gln Leu Gly Ala Leu Glu Gly Tyr Leu His Ser Asp
 245 250 255

Tyr Lys Ala Ile Asn Ser Tyr Leu Arg Asn Asn Arg Val Pro Asn Asn
 260 265 270

Asp Glu Leu Asn Lys Lys Ile Glu Leu Ile Ser Ser Ala Leu Ser Val
 275 280 285

Lys Pro Ile Pro Glu Thr Leu Ile Ala Tyr Arg Arg Val Asp Gly Ile

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290 295 300
 Pro Phe Asp Leu Pro Ser Asp Phe Ser Phe Asp Lys Lys Glu Asn Gly
 305 310 315 320
 Glu Ile Ile Ala Asp Lys Thr Lys Leu Asn Glu Phe Ile Asp Lys Trp
 325 330 335
 Thr Gly Lys Glu Ile Glu Asn Leu Ser Phe Ser Ser Thr Ser Leu Lys
 340 345 350
 Ser Thr Pro Leu Ser Phe Ser Lys Ser Arg Phe Ile Phe Arg Leu Arg
 355 360 365
 Leu Ser Glu Gly Thr Ile Gly Ala Phe Ile Tyr Gly Phe Ser Gly Phe
 370 375 380
 Gln Asp Glu Gln Glu Ile Leu Leu Asn Lys Asn Ser Thr Phe Lys Ile
 385 390 395 400
 Phe Arg Ile Thr Pro Ile Thr Ser Ile Ile Asn Arg Val Thr Lys Met
 405 410 415
 Thr Gln Val Val Ile Asp Ala Glu Val Ile Gln Asn Lys Glu Ile
 420 425 430

 <210> 32
 <211> 721
 <212> PRT
 <213> Protein sequence of Clostridium botulinum C2 toxin component 2

 <400> 32
 Met Leu Val Ser Lys Phe Glu Asn Ser Val Lys Asn Ser Asn Lys Asn
 1 5 10 15
 Tyr Phe Thr Ile Asn Gly Leu Met Gly Tyr Tyr Phe Glu Asn Asp Phe
 20 25 30
 Phe Asn Leu Asn Ile Ile Ser Pro Thr Leu Asp Gly Asn Leu Thr Phe
 35 40 45
 Ser Lys Glu Asp Ile Asn Ser Ile Leu Gly Asn Lys Ile Ile Lys Ser
 50 55 60
 Ala Arg Trp Ile Gly Leu Ile Lys Pro Ser Ile Thr Gly Glu Tyr Ile
 65 70 75 80

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Leu Ser Thr Asn Ser Pro Asn Cys Arg Val Glu Leu Asn Gly Glu Ile
85 90 95

Phe Asn Leu Ser Leu Asn Thr Ser Asn Thr Val Asn Leu Ile Gln Gly
100 105 110

Asn Val Tyr Asp Ile Arg Ile Glu Gln Leu Met Ser Glu Asn Gln Leu
115 120 125

Leu Lys Asn Tyr Glu Gly Ile Lys Leu Tyr Trp Glu Thr Ser Asp Ile
130 135 140

Ile Lys Glu Ile Ile Pro Ser Glu Val Leu Leu Lys Pro Asn Tyr Ser
145 150 155 160

Asn Thr Asn Glu Lys Ser Lys Phe Ile Pro Asn Asn Thr Leu Phe Ser
165 170 175

Asn Ala Lys Leu Lys Ala Asn Ala Asn Arg Asp Thr Asp Arg Asp Gly
180 185 190

Ile Pro Asp Glu Trp Glu Ile Asn Gly Tyr Thr Val Met Asn Gln Lys
195 200 205

Ala Val Ala Trp Asp Asp Lys Phe Ala Ala Asn Gly Tyr Lys Lys Tyr
210 215 220

Val Ser Asn Pro Phe Lys Pro Cys Thr Ala Asn Asp Pro Tyr Thr Asp
225 230 235 240

Phe Glu Lys Val Ser Gly Gln Ile Asp Pro Ser Val Ser Met Val Ala
245 250 255

Arg Asp Pro Met Ile Ser Ala Tyr Pro Ile Val Gly Val Gln Met Glu
260 265 270

Arg Leu Val Val Ser Lys Ser Glu Thr Ile Thr Gly Asp Ser Thr Lys
275 280 285

Ser Met Ser Lys Ser Thr Ser His Ser Ser Thr Asn Ile Asn Thr Val
290 295 300

Gly Ala Glu Val Ser Gly Ser Leu Gln Leu Ala Gly Gly Ile Phe Pro
305 310 315 320

Val Phe Ser Met Ser Ala Ser Ala Asn Tyr Ser His Thr Trp Gln Asn
325 330 335

Thr Ser Thr Val Asp Asp Thr Thr Gly Glu Ser Phe Ser Gln Gly Leu
340 345 350

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Ser Ile Asn Thr Gly Glu Ser Ala Tyr Ile Asn Pro Asn Ile Arg Tyr
 355 360 365

Tyr Asn Thr Gly Thr Ala Pro Val Tyr Asn Val Thr Pro Thr Thr Thr
 370 375 380

Ile Val Ile Asp Lys Gln Ser Val Ala Thr Ile Lys Gly Gln Glu Ser
 385 390 395 400

Leu Ile Gly Asp Tyr Leu Asn Pro Gly Gly Thr Tyr Pro Ile Ile Gly
 405 410 415

Glu Pro Pro Met Ala Leu Asn Thr Met Asp Gln Phe Ser Ser Arg Leu
 420 425 430

Ile Pro Ile Asn Tyr Asn Gln Leu Lys Ser Ile Asp Asn Gly Gly Thr
 435 440 445

Val Met Leu Ser Thr Ser Gln Phe Thr Gly Asn Phe Ala Lys Tyr Asn
 450 455 460

Ser Asn Gly Asn Leu Val Thr Asp Gly Asn Asn Trp Gly Pro Tyr Leu
 465 470 475 480

Gly Thr Ile Lys Ser Thr Thr Ala Ser Leu Thr Leu Ser Phe Ser Gly
 485 490 495

Gln Thr Thr Gln Val Ala Val Val Ala Pro Asn Phe Ser Asp Pro Glu
 500 505 510

Asp Lys Thr Pro Lys Leu Thr Leu Glu Gln Ala Leu Val Lys Ala Phe
 515 520 525

Ala Leu Glu Lys Lys Asn Gly Lys Phe Tyr Phe His Gly Leu Glu Ile
 530 535 540

Ser Lys Asn Glu Lys Ile Gln Val Phe Leu Asp Ser Asn Thr Asn Asn
 545 550 555 560

Asp Phe Glu Asn Gln Leu Lys Asn Thr Ala Asp Lys Asp Ile Met His
 565 570 575

Cys Ile Ile Lys Arg Asn Met Asn Ile Leu Val Lys Val Ile Thr Phe
 580 585 590

Lys Glu Asn Ile Ser Ser Ile Asn Ile Ile Asn Asp Thr Asn Phe Gly
 595 600 605

Val Gln Ser Met Thr Gly Leu Ser Asn Arg Ser Lys Gly Gln Asp Gly

